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OM protein - protein search, using sw model

Run on: November 8, 2004, 08:05:27 ; Search time 44.8163 Seconds
(without alignments)
3132.595 Million cell updates/sec

Title: US-09-830-693B-27
Perfect score: 1250
Sequence: 1 SLALSLTADQMVSALLDAEP.....CKNVVPLYDLLLEMLDAHRL 244

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1239.5	99.2	595	1 ESR1_HUMAN	P03372 homo sapien
2	1205.5	96.4	596	2 Q6QIS5	Q6qis5 bos taurus
3	1205.5	96.4	596	2 AAS46251	Aas46251 bos taurus
4	1204.5	96.4	599	1 ESR1_MOUSE	P19785 mus musculus
5	1200.5	96.0	600	1 ESR1_RAT	P06211 rattus norv
6	1197.5	95.8	595	1 ESR1_PIG	Q29040 sus scrofa
7	1192.5	95.4	595	1 ESR1_MESAU	Q9qzj5 mesocricetu
8	1179.5	94.4	587	2 Q8UWB0	Q8uwb0 caiman croc
9	1179	94.3	594	1 ESR1_HORSE	Q9tv98 equus cabal
10	1177.5	94.2	587	1 ESR1_POEGU	Q91250 poephila gu
11	1176.5	94.1	589	1 ESR1_CHICK	P06212 gallus gall
12	1175.5	94.0	587	2 Q765N7	Q765n7 alligator m
13	1175.5	94.0	587	2 BAD08348	Bad08348 alligator
14	1172.5	93.8	589	2 Q8AYH0	Q8ayh0 coturnix co
15	1170.5	93.6	353	2 Q8CGK8	Q8cgc8 cavia porce
16	1164.5	93.2	431	2 Q95L13	Q95l13 ovis aries
17	1140.5	91.2	581	2 Q8UWA9	Q8uwa9 cnemidophor
18	1133.5	90.7	349	1 ESR1_ANOCA	Q9yht3 anolis caro
19	1071.5	85.7	427	2 Q6W5G5	Q6w5g5 xenopus lae
20	1071.5	85.7	427	2 AAQ84784	Aaq84784 xenopus l
21	1071.5	85.7	543	2 Q6W5G9	Q6w5g9 xenopus tro
22	1071.5	85.7	543	2 AAQ84780	Aaq84780 xenopus t
23	1071.5	85.7	585	2 Q6W5G7	Q6w5g7 xenopus lae
24	1071.5	85.7	585	2 AAQ84782	Aaq84782 xenopus l
25	1066.5	85.3	586	1 ESR1_XENLA	P81559 xenopus lae
26	1062.5	85.0	427	2 Q6W5G6	Q6w5g6 xenopus lae
27	1062.5	85.0	427	2 AAQ84783	Aaq84783 xenopus l
28	1025.5	82.0	307	1 ESR1_CNEUN	Q91424 cnemidophor
29	861.5	68.9	174	1 ESR1_BOVIN	P49884 bos taurus
30	824.5	66.0	570	2 Q800Q2	Q800q2 zoarces viv
31	820.5	65.6	574	2 Q7T2K8	Q7t2k8 halichoeres

32	820.5	65.6	627	2	Q9DDZ4	Q9ddz4 micropterus
33	820.5	65.6	627	2	AAG44622	Aag44622 micropter
34	818	65.4	542	2	Q90ZE6	Q90ze6 squalus aca
35	812.5	65.0	620	2	Q7SZI0	Q7szio fundulus he
36	809.5	64.8	581	1	ESR1_PAGMA	O42132 pagrus majo
37	808.5	64.7	525	1	ESR1_MICUN	P57753 micropogoni
38	808.5	64.7	579	1	ESR1_SPAAU	Q9pv29 sparus aura
39	804.5	64.4	620	1	ESR1_ORYLA	P50241 oryzias lat
40	801.5	64.1	583	2	Q804Q6	Q804q6 acanthopagr
41	801.5	64.1	622	1	ESR1_ONCMY	P16058 oncorhynch
42	798.5	63.9	585	1	ESR1_ORENI	Q9yh33 oreochromis
43	797.5	63.8	535	1	ESR1_SALSA	P50242 salmo salar
44	797	63.8	578	2	Q8QHL0	Q8qhl0 paralichthy
45	794.5	63.6	569	1	ESR1_BRARE	P57717 brachydanio

ALIGNMENTS

RESULT 1
ESR1_HUMAN STANDARD; PRT; 595 AA.
AC P03372; Q13511; Q14276; Q9NU51; Q9UD27; Q9UIS7;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
GN Name=ESR1; Synonyms=NR3A1, ESR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX MEDLINE=86122927; PubMed=3753802;
RA Greene G.L., Gilna P., Waterfield M., Baker A., Hort Y., Shine J.;
RT "Sequence and expression of human estrogen receptor complementary
RT DNA.";
RL Science 231:1150-1154(1986).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX MEDLINE=86146892; PubMed=3754034;
RA Green S., Walter P., Kumar V., Krust A., Bornert J.-M., Argos P.,
RA Chambon P.;
RT "Human oestrogen receptor cDNA: sequence, expression and homology to
RT v-erb-A.";
RL Nature 320:134-139(1986).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANT ASP-411 INS.
RC TISSUE=Breast;
RX MEDLINE=96174665; PubMed=8600466;
RA Pink J.J., Wu S.Q., Wolf D.M., Bilimoria M.M., Jordan V.C.;
RT "A novel 80 kDa human estrogen receptor containing a duplication of
RT exons 6 and 7.";
RL Nucleic Acids Res. 24:962-969(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANT SER-77.
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 152-595 FROM N.A. (ISOFORM LONG).
RX MEDLINE=20084372; PubMed=10619354;
RA Schubert E.L., Lee M.K., Newman B., King M.C.;
RT "Single nucleotide polymorphisms (SNPs) in the estrogen receptor gene
RT and breast cancer susceptibility.";
RL J. Steroid Biochem. Mol. Biol. 71:21-27(1999).
RN [6]
RP SEQUENCE OF 216-434 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Breast carcinoma;

RX MEDLINE=93153765; PubMed=7916651;
RA Pfeiffer U., Pecarotta E., Castagnetta L., Vidali G.;
RT "Estrogen receptor variant messenger RNA lacking exon 4 in estrogen-
RT responsive human breast cancer cell lines.";
RL Cancer Res. 53:741-743(1993).
RN [7]
RP SEQUENCE OF 110-117, PHOSPHORYLATION, AND MUTAGENESIS.
RX MEDLINE=96026869; PubMed=7476978;
RA Joel P.B., Traish A.M., Lannigan D.A.;
RT "Estradiol and phorbol ester cause phosphorylation of serine 118 in
RT the human estrogen receptor.";
RL Mol. Endocrinol. 9:1041-1052(1995).
RN [8]
RP SEQUENCE OF 354-548 FROM N.A.
RC TISSUE=Breast carcinoma;
RA Naundorf H., Becker M., Fiebig C., Buettner B., Fichtner I.;
RT "Mechanisms of acquired tamoxifen resistance in a xenotransplanted
RT human breast carcinoma.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE OF 413-595 FROM N.A.
RA Parker A.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE OF 532-542, AND PHOSPHORYLATION.
RX MEDLINE=95280953; PubMed=7539106;
RA Arnold S.F., Obourn J.D., Jaffe H., Notides A.C.;
RT "Phosphorylation of the human estrogen receptor on tyrosine 537 in
RT vivo and by src family tyrosine kinases in vitro.";
RL Mol. Endocrinol. 9:24-33(1995).
RN [11]
RP INTERACTION WITH NCOA6.
RX MEDLINE=20036574; PubMed=10567404;
RA Lee S.-K., Anzick S.L., Choi J.-E., Bubendorf L., Guan X.-Y.,
RA Jung Y.-K., Kallioniemi O.P., Kononen J., Trent J.M., Azorsa D.,
RA Junn B.-H., Cheong J.H., Lee Y.C., Meltzer P.S., Lee J.W.;
RT "A nuclear factor ASC-2, as a cancer-amplified transcriptional
RT coactivator essential for ligand-dependent transactivation by nuclear
RT receptors in vivo.";
RL J. Biol. Chem. 274:34283-34293(1999).
RN [12]
RP INTERACTION WITH NCOA5.
RX MEDLINE=20565767; PubMed=11132208; DOI=10.1128/MCB.21.1.343-353.2001;
RA Sauve F., McBroom L.D.B., Gallant J., Moraitis A.N., Labrie F.,
RA Giguere V.;
RT "CIA, a novel estrogen receptor coactivator with a bifunctional
RT nuclear receptor interacting determinant.";
RL Mol. Cell. Biol. 21:343-353(2001).
RN [13]
RP PHOSPHORYLATION.
RX MEDLINE=95140025; PubMed=7838153;
RA Arnold S.F., Obourn J.D., Jaffe H., Notides A.C.;
RT "Serine 167 is the major estradiol-induced phosphorylation site on the
RT human estrogen receptor.";
RL Mol. Endocrinol. 8:1208-1214(1994).
RN [14]
RP PHOSPHORYLATION SITES SER-104 AND SER-106, AND MUTAGENESIS.
RX MEDLINE=99357754; PubMed=10428798;
RA Rogatsky I., Trowbridge J.M., Garabedian M.J.;
RT "Potentiation of human estrogen receptor alpha transcriptional
RT activation through phosphorylation of serines 104 and 106 by the
RT cyclin A-CDK2 complex.";
RL J. Biol. Chem. 274:22296-22302(1999).
RN [15]
RP STRUCTURE BY NMR OF 180-262.
RX MEDLINE=91061891; PubMed=2247153;
RA Schwabe J.W.E., Neuhaus D., Rhodes D.;
RT "Solution structure of the DNA-binding domain of the oestrogen
RT receptor.";
RL Nature 348:458-461(1990).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 180-262.
RX MEDLINE=94037103; PubMed=8221895;
Schwabe J.W.E., Chapman L., Finch J.T., Rhodes D.;
RT "The crystal structure of the estrogen receptor DNA-binding domain
RT bound to DNA: how receptors discriminate between their response
RT elements.";
RL Cell 75:567-578(1993).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF 305-548.
RX MEDLINE=97478539; PubMed=9338790;
RA Brzozowski A.M., Pike A.C.W., Dauter Z., Hubbard R.E., Bonn T.,
RA Engstrom O., Oehman L., Greene G.L., Gustafsson J.-A., Carlquist M.;
RT "Molecular basis of agonism and antagonism in the oestrogen
RT receptor.";
RL Nature 389:753-758(1997).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 306-544.
RX MEDLINE=98263297; PubMed=9600906;
RA Tanenbaum D.M., Wang Y., Williams S.P., Sigler P.B.;
RT "Crystallographic comparison of the estrogen and progesterone
RT receptor's ligand binding domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:5998-6003(1998).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (1.90 ANGSTROMS) OF 294-554.
RX MEDLINE=99091051; PubMed=9875847;
RA Shiau A.K., Barstad D., Loria P.M., Cheng L., Kushner P.J.,
RA Agard D.A., Greene G.L.;
RT "The structural basis of estrogen receptor/coactivator recognition and
RT the antagonism of this interaction by tamoxifen.";
RL Cell 95:927-937(1998).
RN [20]
RP 3D-STRUCTURE MODELING OF 311-547.
RX MEDLINE=98280806; PubMed=9619507;
RA Maalouf G.J., Xu W., Smith T., Mohr S.C.;
RT "Homology model for the ligand-binding domain of the human estrogen
RT receptor.";
RL J. Biomol. Struct. Dyn. 15:841-850(1998).
RN [21]
RP VARIANT VAL-400.
RX MEDLINE=9005402; PubMed=2792078;
RA Tora L., Mullick A., Metzger D., Ponglikitmongkol M., Park I.,
RA Chambon P.;
RT "The cloned human oestrogen receptor contains a mutation which alters
RT its hormone binding properties.";
RL EMBO J. 8:1981-1986(1989).
RN [22]
RP VARIANT ALA-447.
RX MEDLINE=92250650; PubMed=1577818;
RA Reese J.C., Katzenellenbogen B.S.;
RT "Characterization of a temperature-sensitive mutation in the hormone
RT binding domain of the human estrogen receptor. Studies in cell
RT extracts and intact cells and their implications for hormone-dependent
RT transcriptional activation.";
RL J. Biol. Chem. 267:9868-9873(1992).
RN [23]
RP VARIANT GLU-364.
RX MEDLINE=97120591; PubMed=8961262;
RA McInerney E.M., Ince B.A., Shapiro D.J., Katzenellenbogen B.S.;
RT "A transcriptionally active estrogen receptor mutant is a novel type
RT of dominant negative inhibitor of estrogen action.";
RL Mol. Endocrinol. 10:1519-1526(1996).
RN [24]
RP VARIANT CYS-160.
RX MEDLINE=97338667; PubMed=9195227;
RA Anderson T.I., Wooster R., Laake K., Collins N., Warren W., Skrede M.,
RA Eeles R., Tveit K.M., Johnston S.R.D., Dowsett M., Olsen A.O.,
RA Moeller P., Stratton M.R., Boerresen-Dale A.-L.;
RT "Screening for ESR mutations in breast and ovarian cancer patients.";
RL Hum. Mutat. 9:531-536(1997).
CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their
CC receptors are involved in the regulation of eukaryotic gene
CC expression and affect cellular proliferation and differentiation
CC in target tissues.
CC -!- SUBUNIT: Binds DNA as a homodimer. Binds UBE1C (By similarity).
CC Can form a heterodimer with ESR2. Interacts with NCOA3, NCOA5 and

CC NCOA6 coactivators, leading to a strong increase of transcription
CC of target genes.

Query Match 99.2%; Score 1239.5; DB 1; Length 595;
Best Local Similarity 99.6%; Pred. No. 1.7e-95;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY	1	SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV	60
Dd	305	SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV	364
QY	61	PGFVDLTLHDQVHLLECAWL EILMIGLVWRSM EHPGKLLFAPNLLLDNRNQKCKVEGMVEI	120
Dd	365	PGFVDLTLHDQVHLLECAWL EILMIGLVWRSM EHPGKLLFAPNLLLDNRNQKCKVEGMVEI	424
QY	121	FDMLLATSSRRFRMN LQG-EFVLKSI ILLNSGVYTFLSSTLKSL EKDHIHRVLDKITD	179
Dd	425	FDMLLATSSRRFRMN LQGE EFVCLKSI ILLNSGVYTFLSSTLKSL EKDHIHRVLDKITD	484
QY	180	TLIHLMAKAGLTQQQHQR LAQLLL ILSHIRHMSNKGM EHYLSMKCKNVVP LYDLLLEML	239
Dd	485	TLIHLMAKAGLTQQQHQR LAQLLL ILSHIRHMSNKGM EHYLSMKCKNVVP LYDLLLEML	544
QY	240	DAHRL 244	
Dd	545	DAHRL 549	

RESULT 2

Q6QIS5 PRELIMINARY; PRT; 596 AA.

ID	Q6QIS5	(TrEMBLrel. 27, Created)	
AC	Q6QIS5;		
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	Estrogen receptor alpha.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Uterus;		
RA	Nishimura N., Tetsuka M.;		
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.		
CC	-!- SUBCELLULAR LOCATION: Nuclear (By similarity).		
CC	-!- SIMILARITY: Belongs to the nuclear hormone receptor family.		
DR	EMBL; AY538775; AAS46251.1; -		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	InterPro; IPR000536; Hrmn_recept_lig.		
DR	InterPro; IPR001292; Oestrgn_receptor.		
DR	InterPro; IPR001723; Stdhrmn_receptor.		
DR	InterPro; IPR008946; Str_ncl_receptor.		
DR	InterPro; IPR001628; Znf_C4steroid.		
DR	Pfam; PF00104; Hormone_recep; 1.		
DR	Pfam; PF02159; Oest_recep; 1.		
DR	Pfam; PF00105; zf-C4; 1.		
DR	PRINTS; PR00543; OESTROGENR.		
DR	PRINTS; PR00398; STRDHORMONER.		
DR	PRINTS; PR00047; STROIDFINGER.		
DR	ProDom; PD000035; Znf_C4steroid; 1.		
DR	SMART; SM00430; HOLI; 1.		
DR	SMART; SM00399; Znf_C4; 1.		
DR	PROSITE; PS00031; NUCLEAR RECEPTOR; 1.		
KW	DNA-binding; Metal-binding; Nuclear protein; Receptor;		
KW	Transcription regulation; Zinc; Zinc-finger.		
SQ	SEQUENCE 596 AA; 66489 MW; 3E2CE85BE7844FF2 CRC64;		

DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
GN Name=Esrl; Synonyms=Nr3a1, ESR, Estr, EstrA;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=91042558; PubMed=2484714;
RA White R., Lees J.A., Needham M., Ham J., Parker M.;
RT "Structural organization and expression of the mouse estrogen
RT receptor.";
RL Mol. Endocrinol. 1:735-744(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Bone, and Thymus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Kazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaïdo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 20,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE OF 1-22 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20359284; PubMed=10899303;
RA Kos M., O'Brien S., Flouriot G., Gannon F.;
RT "Tissue-specific expression of multiple mRNA variants of the mouse
RT estrogen receptor alpha gene.";
RL FEBS Lett. 477:15-20(2000).
RN [4]
RP SEQUENCE OF 269-599 FROM N.A.
RC STRAIN=SJL/J, and B10.S/J; TISSUE=Spleen;
RA Ma R.Z., Teuscher C.;
RT "Screening for candidate genes of mouse autoimmune diseases.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP CARBOHYDRATE-LINKAGE SITE SER-575.
RX MEDLINE=97153020; PubMed=8999954;
RA Jiang M.S., Hart G.W.;
RT "A subpopulation of estrogen receptors are modified by O-linked N-
RT acetylglucosamine.";
RL J. Biol. Chem. 272:2421-2428(1997).
RN [6]
RP CARBOHYDRATE-LINKAGE SITES SER-10; THR-50 AND SER-575.
RX MEDLINE=21124487; PubMed=11226831;

RA Cheng X., Hart G.W.;
RT "Glycosylation of the murine estrogen receptor-alpha.";
RL J. Steroid Biochem. Mol. Biol. 75:147-158(2000).
RN [7]
RP INTERACTION WITH NCOA3.
RX MEDLINE=97336097; PubMed=9192892;
RA Torchia J., Rose D.W., Inostroza J., Kamei Y., Westin S., Glass C.K.,
RA Rosenfeld M.G.;
RT "The transcriptional co-activator p/CIP binds CBP and mediates
RT nuclear-receptor function.";
RL Nature 387:677-684(1997).
RN [8]
RP INTERACTION WITH NCOA6.
RX MEDLINE=20250907; PubMed=10788465;
RA Zhu Y.-J., Kan L., Qi C., Kanwar Y.S., Yeldandi A.V., Rao M.S.,
RA Reddy J.K.;
RT "Isolation and characterization of peroxisome proliferator-activated
RT receptor (PPAR) interacting protein (PRIP) as a coactivator for
RT PPAR.";
RL J. Biol. Chem. 275:13510-13516(2000).
CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their
CC receptors are involved in the regulation of eukaryotic gene
CC expression and affect cellular proliferation and differentiation
CC in target tissues.
CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with
CC ESR2. Interacts with NCOA3 and NCOA6 coactivators, leading to a
CC strong increase of transcription of target genes. Interacts with
CC NCOA5. Binds UBE1C (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- PTM: Phosphorylated by cyclin A/CDK2 (By similarity).
CC -!- MISCELLANEOUS: In the absence of ligand, steroid hormone receptors
CC are thought to be weakly associated with nuclear components;
CC hormone binding greatly increases receptor affinity. The hormone-
CC receptor complex appears to recognize discrete DNA sequences
CC upstream of transcriptional start sites.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; M38651; AAA37580.1; -.
DR EMBL; AK036627; BAC29510.1; -.
DR EMBL; AK041525; BAC30973.1; -.
DR EMBL; AJ276597; CAB85618.1; -.
DR EMBL; AF128221; AAF22562.1; -.
DR EMBL; AF128220; AAF22561.1; -.
DR PIR; A40061; QRMSE.
DR HSSP; P03372; LHCP.
DR TRANSFAC; T00259; -.
DR GlycoSuiteDB; P19785; -.
DR MGD; MGI:1352467; Esrl.
DR GO; GO:0016585; C:chromatin remodeling complex; ISS.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0016020; C:membrane; ISS.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0030284; F:estrogen receptor activity; ISS.
DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.
DR GO; GO:0016049; P:cell growth; NAS.
DR GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.
DR GO; GO:0045839; P:negative regulation of mitosis; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
DR InterPro; IPR000536; Hrmn_recept_lig.
DR InterPro; IPR001292; Oestrgn_receptor.
DR InterPro; IPR001723; Stdhrmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.

QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMVEI 120
Db 365 PGFLDLSLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMVEI 424
QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFSLSTLKSLEEKDHIHRVLDKITD 179
Db 425 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFSLSTLKSLEEKDHIHRVLDKITD 484
QY 180 TLIHLMKAGLTQQQHRRLAQQLLLSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 239
Db 485 TLIHLMKAGLTQQQHRRLAQQLLLSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 544
QY 240 DAHRL 244
Db 545 DAHRL 549

RESULT 7
ESTRAGON MESAU STANDARD; PRT; 595 AA.
ID Q9QZJ5; Q9QZG6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
GN Name=ESR1; Synonyms=NR3A1, ESR;
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=20197937; PubMed=10731637;
RA Bhat H.K., Vadgama J.V.;
RT "Hamster estrogen receptor cDNA: cloning and mRNA expression.";
RL J. Steroid Biochem. Mol. Biol. 72:47-53 (2000).
RN [2]
RP SEQUENCE OF 98-291 FROM N.A.
RA Jones J.E., Carpenter C.D., Lubbers L.S., Petersen S.L., Wade G.N.;
RT "Return of lordosis after food deprivation and refeeding in Syrian hamsters.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues (By similarity).
CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ESR2. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading to a strong increase of transcription of target genes. Binds UBE1C (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3 subfamily.
CC -----
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CC -----
CC EMBL; AF181077; AAD53956.1; -.
CC EMBL; AF184276; AAF02721.1; -.
CC HSSP; P03372; 1HCO.
CC GO; GO:0016585; C:chromatin remodeling complex; ISS.
CC GO; GO:0016020; C:membrane; ISS.
CC GO; GO:0030284; F:estrogen receptor activity; ISS.

DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.
DR GO; GO:0016049; P:cell growth; ISS.
DR GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.
DR GO; GO:0045839; P:negative regulation of mitosis; ISS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
DR InterPro; IPR000536; Hmon_recept_lig.
DR InterPro; IPR001292; Oestrgn_receptor.
DR InterPro; IPR001723; Stchrnm_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF02159; Oest_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00543; OESTROGENR.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Phosphorylation; Receptor;
KW Steroid-binding; Transcription regulation; Zinc-finger.
FT DOMAIN 1 184 Modulating.
FT DNA_BIND 185 250 Nuclear receptor-type.
FT ZN_FING 185 205 C4-type.
FT ZN_FING 221 245 C4-type.
FT DOMAIN 251 310 Hinge.
FT DOMAIN 311 551 Steroid-binding.
FT DOMAIN 112 115 Poly-Pro.
FT DOMAIN 166 169 Poly-Ser.
FT MOD_RES 103 103 Phosphoserine (by CDK2) (By similarity).
FT MOD_RES 105 105 Phosphoserine (by CDK2) (By similarity).
FT MOD_RES 118 118 Phosphoserine (By similarity).
FT MOD_RES 167 167 Phosphoserine (by CK2) (By similarity).
FT MOD_RES 537 537 Phosphotyrosine (by Tyr-kinases) (By similarity).
FT CONFLICT 98 99 QL -> PF (in Ref. 2).
FT CONFLICT 144 144 S -> T (in Ref. 2).
FT CONFLICT 198 199 GV -> EVEQI (in Ref. 2).
FT CONFLICT 290 291 NL -> KG (in Ref. 2).
SQ SEQUENCE 595 AA; 66833 MW; E4D803B4FFDB257E CRC64;

Query Match 95.4%; Score 1192.5; DB 1; Length 595;
Best Local Similarity 94.7%; Pred. No. 1.5e-91;
Matches 232; Conservative 8; Mismatches 4; Indels 1; Gaps 1;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SPALSLTADQMVSAALLDAEPPILYSEYDPTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMVEI 120
Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMVEI 424
QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFSLSTLKSLEEKDHIHRVLDKITD 179
Db 425 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFSLSTLKSLEEKDHIHRVLDKITD 484
QY 180 TLIHLMKAGLTQQQHRRLAQQLLLSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 239
Db 485 TLIHLMKAGLTQQQHRRLAQQLLLSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 544
QY 240 DAHRL 244
Db 545 DAHRL 549
RESULT 8
Q8UWB0
ID Q8UWB0 PRELIMINARY; PRT; 587 AA.
AC Q8UWB0;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)

RL EMBO J. 5:891-897(1986).

CC -!- FUNCTION: The steroid hormones and their receptors are involved in

CC the regulation of eukaryotic gene expression and affect cellular

CC proliferation and differentiation in target tissues.

CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ER-

CC beta.

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,

CC a DNA-binding domain and a C-terminal steroid-binding domain.

CC -!- MISCELLANEOUS: In the absence of ligand, steroid hormone receptors

CC are thought to be weakly associated with nuclear components;

CC hormone binding greatly increases receptor affinity. The hormone-

CC receptor complex appears to recognize discrete DNA sequences

CC upstream of transcriptional start sites.

CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3

CC subfamily.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; X03805; CAA27433.1; -.

DR PIR; A0914; QRCHE.

DR HSSP; P03372; LHCP.

DR TRANSFAC; T00264; -.

DR GO; GO:0016585; C:chromatin remodeling complex; ISS.

DR GO; GO:0016020; C:membrane; ISS.

DR GO; GO:0030284; F:estrogen receptor activity; ISS.

DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.

DR GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.

DR InterPro; IPR000536; Hrmn_recept_lig.

DR InterPro; IPR001292; Oestrn_receptor.

DR InterPro; IPR001723; Stdhrmn_receptor.

DR InterPro; IPR008946; Str_ncl_receptor.

DR InterPro; IPR001628; Znf_C4steroid.

DR Pfam; PF00104; Hormone_recep; 1.

DR Pfam; PF02159; Oest_recep; 1.

DR Pfam; PF00105; zf-C4; 1.

DR PRINTS; PR00543; OESTROGENR.

DR PRINTS; PR00398; STRDHORMONER.

DR PRINTS; PR00047; STROIDFINGER.

DR ProDom; PD000035; Znf_C4steroid; 1.

DR SMART; SM00430; HOLI; 1.

DR SMART; SM00399; Znf_C4; 1.

DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

DR DNA-binding; Nuclear protein; Receptor; Steroid-binding;

KW Transcription regulation; Zinc-finger.

FT DOMAIN 1 178 Modulating.

FT DNA_BIND 179 244 Nuclear receptor-type.

FT ZN_FING 179 199 C4-type.

FT ZN_FING 215 239 C4-type.

FT DOMAIN 245 304 Hinge.

FT DOMAIN 305 589 Steroid-binding.

SQ SEQUENCE 589 AA; 66746 MW; 1B092233C770A54B CRC64;

Query Match 94.1%; Score 1176.5; DB 1; Length 589;

Best Local Similarity 93.5%; Pred. No. 3.3e-90;

Matches 229; Conservative 12; Mismatches 3; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMVSAALDAEPPILYSEYDPTRPFEASMMGLLTNLADRELVHMINWAKRV 60

Db 299 SPALSLTAEQMVSAALAEPPIVYSEYDPNRPFNEASMMTLLTNLADRELVHMINWAKRV 358

Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCKVEGMVEI 120

Db 359 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCKVEGMVEI 418

Qy 121 FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179

Db 419 FDMLLATAARFRMMNLQGEFEVCLKSIILLNSGVYTFLSSTLKSLEERDIHRVLDKITD 478

Qy 180 TLIHLMKAGLTQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 239

Db 479 TLIHLMKAGLSLQQHRRRLAQLLLILSHIRHMSNKGMEHLYNMKCKNVVPLYDLLLEML 538

Qy 240 DAHRL 244

Db 539 DAHRL 543

RESULT 12

Q765N7

ID Q765N7 PRELIMINARY; PRT; 587 AA.

AC Q765N7;

DT 05-JUL-2004 (TremBLrel. 27, Created)

DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)

DE Estrogen receptor a.

GN Name=ERA;

OS Alligator mississippiensis (American alligator).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Crocodyliidae; Alligatorinae; Alligator.

OX NCBI_TaxID=8496;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Gonad;

RX PubMed=14980803;

RA Katsu Y., Bermudez D.S., Braun E.L., Helbing C., Miyagawa S.,

RA Gunderson M.P., Kohno S., Bryan T.A., Guillette L.J., Iguchi T.;

RT "Molecular cloning of the estrogen and progesterone receptors of the

RT American alligator.";

RL Gen. Comp. Endocrinol. 136:122-133(2004).

CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.

DR EMBL; AB115909; BAD08348.1; -.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR000536; Hrmn_recept_lig.

DR InterPro; IPR001292; Oestrn_receptor.

DR InterPro; IPR001723; Stdhrmn_receptor.

DR InterPro; IPR008946; Str_ncl_receptor.

DR InterPro; IPR001628; Znf_C4steroid.

DR Pfam; PF00104; Hormone_recep; 1.

DR Pfam; PF02159; Oest_recep; 1.

DR Pfam; PF00105; zf-C4; 1.

DR PRINTS; PR00543; OESTROGENR.

DR PRINTS; PR00398; STRDHORMONER.

DR PRINTS; PR00047; STROIDFINGER.

DR ProDom; PD000035; Znf_C4steroid; 1.

DR SMART; SM00430; HOLI; 1.

DR SMART; SM00399; Znf_C4; 1.

DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

KW DNA-binding; Metal-binding; Nuclear protein; Receptor;

KW Transcription regulation; Zinc; Zinc-finger.

SQ SEQUENCE 587 AA; 66497 MW; FC217FCC0F1B41F0 CRC64;

Query Match 94.0%; Score 1175.5; DB 2; Length 587;

Best Local Similarity 93.5%; Pred. No. 4e-90;

Matches 229; Conservative 12; Mismatches 3; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMVSAALDAEPPILYSEYDPTRPFEASMMGLLTNLADRELVHMINWAKRV 60

Db 299 SPALSLTAEQMVSAALAEPPIVYSEYDPNRPFNEASMMTLLTNLADRELVHMINWAKRV 358

Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCKVEGMVEI 120

Db 359 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCKVEGMVEI 418

Qy 121 FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179

Db 419 FDMLLATAARFRMMNLQGEFEVCLKSIILLNSGVYTFLSSTLKSLEEKDIHRVLDKITD 478

Search completed: November 8, 2004, 08:27:59
 Job time : 46.8163 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 8, 2004, 08:14:27 ; Search time 11.951 Seconds
(without alignments)
1964.426 Million cell updates/sec

Title: US-09-830-693B-27
Perfect score: 1250
Sequence: 1 SLALSLTADQMVSALLDAEP.....CKNVVPLYDLLLEMLDAHRL 244

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1230.5	98.4	595	1 QRHUE	estrogen receptor
2	1204.5	96.4	599	1 QRMSE	estrogen receptor
3	1200.5	96.0	600	1 QRRTE	estrogen receptor
4	1197.5	95.8	595	2 I47140	estradiol receptor
5	1177.5	94.2	701	2 S64737	80K estrogen recep
6	1176.5	94.1	589	1 QRCHE	estrogen receptor
7	1066.5	85.3	586	1 QRXLE	estrogen receptor
8	804.5	64.4	620	2 T10423	estrogen receptor
9	797.5	63.8	535	2 S58224	estrogen receptor
10	774.5	62.0	574	2 A37197	estrogen receptor
11	759.5	60.8	477	2 S71400	estrogen receptor
12	759.5	60.8	530	2 JC5939	estrogen receptor
13	746.5	59.7	503	2 JW0046	estrogen receptor
14	659.5	52.8	133	2 S26595	estrogen receptor
15	580.5	46.4	121	2 I67419	estradiol receptor
16	366.5	29.3	433	2 B29345	steroid hormone re
17	346.5	27.7	433	2 S58087	estrogen receptor
18	309	24.7	521	2 A29345	steroid hormone re
19	260.5	20.8	758	2 S60586	glucocorticoid rec
20	250	20.0	930	2 A25923	progesterone recep
21	249	19.9	933	1 QRHUP	progesterone recep
22	247.5	19.8	467	2 A43781	retinoid-X-recepto
23	246.5	19.7	786	2 A35466	progesterone recep
24	246	19.7	923	2 A39596	progesterone recep
25	245	19.6	923	2 I53280	progesterone recep
26	242	19.4	441	2 I50515	retinoid X recepto
27	240.5	19.2	488	2 C41977	retinoid acid rece
28	238.5	19.1	463	2 S26670	retinoid acid rece
29	238.5	19.1	463	2 B41727	retinoid-X recepto

30	236.5	18.9	462	1 S09592	retinoid X recepto
31	236	18.9	467	2 S26668	retinoic acid rece
32	236	18.9	467	2 A47278	retinoid X recepto
33	232.5	18.6	470	2 D41977	retinoid receptor
34	230.5	18.4	771	2 A54273	glucocorticoid rec
35	228.5	18.3	379	2 I50514	retinoid X recepto
36	225	18.0	533	2 S37781	retinoid X recepto
37	224	17.9	410	2 S26669	retinoic acid rece
38	224	17.9	446	2 A34418	H-2 region II bind
39	224	17.9	448	2 D41727	retinoid X recepto
40	224	17.9	451	2 A41651	retinoic acid rece
41	224	17.9	520	2 I84718	RXR-beta1 isoform
42	223.5	17.9	777	1 QRHUGA	glucocorticoid rec
43	223.5	17.9	783	1 A25691	glucocorticoid rec
44	223.5	17.9	848	2 JG0194	androgen receptor
45	222.5	17.8	742	1 QRHUGB	glucocorticoid rec

ALIGNMENTS

RESULT 1

QRHUE

estrogen receptor 1 - human
N;Alternate names: ER1; estrogen receptor alpha
C;Species: Homo sapiens (man)

C;Date: 28-May-1986 #sequence revision 28-May-1986 #text change 09-Jul-2004
C;Accession: A94284; A93376; A43021; S27143; S34000; A41925; A03244; C41925; D41
R;Greene, G.L.; Gilna, P.; Waterfield, M.; Baker, A.; Hort, Y.; Shine, J.
Science 231, 1150-1154, 1986

A;Title: Sequence and expression of human estrogen receptor complementary DNA.
A;Reference number: A94284; MUID:86122927; PMID:3753802

A;Accession: A94284

A;Molecule type: mRNA

A;Residues: 1-595 <GR1>

A;Cross-references: UNIPROT:Q14268; UNIPROT:Q9UE35; GB:M12674; NID:g182192; PIDN:AAAS239
R;Green, S.; Walter, P.; Kumar, V.; Krust, A.; Bornert, J.M.; Argos, P.; Chambon, P.
Nature 320, 134-139, 1986

A;Title: Human oestrogen receptor cDNA: sequence, expression and homology to v-erb-A.
A;Reference number: A93376; MUID:86146892; PMID:3754034

A;Accession: A93376

A;Molecule type: mRNA

A;Residues: 1-595 <GR2>

A;Cross-references: GB:X03635; NID:g31233; PIDN:CAA27284.1; PID:g31234
R;Ponglikitmongkol, M.; Green, S.; Chambon, P.
EMBO J. 7, 3385-3388, 1988

A;Title: Genomic organization of the human oestrogen receptor gene.
A;Reference number: A43021; MUID:89091079; PMID:3145193

A;Accession: A43021

A;Molecule type: DNA

A;Residues: 143-161;205-225;244-264;356-374,'G',376;402-422;447-460,'P',462-467;508-528
R;Keaveney, M.; Klug, J.; Gannon, F.
DNA Seq. 2, 347-358, 1992

A;Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene
A;Reference number: S27140; MUID:93075998; PMID:1476547

A;Accession: S27143

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-115 <KEA>

A;Cross-references: EMBL:X62462; NID:g31201; PIDN:CAA44322.1; PID:g31205
R;Pfeffer, U.; Fecarotta, E.; Castagnetta, L.; Vidali, G.
Cancer Res. 53, 741-743, 1993

A;Title: Estrogen receptor variant messenger RNA lacking exon 4 in estrogen-responsive h
A;Reference number: S34000; MUID:93153765; PMID:7916651

A;Accession: S34000

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 216-254,367-399,'G',401-434 <PFE>

A;Cross-references: EMBL:X73067; NID:g579865; PIDN:CAA51528.1; PID:g939886
A;Note: the authors translated the codon GGG for residue 400 as Val

R;Dotzlaw, H.; Alkhalaf, M.; Murphy, L.C.
Mol. Endocrinol. 6, 773-785, 1992

A;Title: Characterization of estrogen receptor variant mRNAs from human breast cancers.

A;Reference number: A41925; MUID:92293154; PMID:1603086
A;Accession: A41925
A;Molecule type: mRNA
A;Residues: 1-214,'ELPTLC' <DOT>
A;Cross-references: GB:M69297; NID:g182218; PIDN:AAA58462.1; PID:g182219
A;Experimental source: clone 4; breast cancer
A;Note: sequence has been revised after extraction from NCBI backbone
A;Note: the complete sequence of neither the nucleotide nor the protein is shown in this
A;Note: sequence extracted from NCBI backbone (NCBIN:106580)
A;Accession: B41925
A;Status: significant sequence differences
A;Molecule type: mRNA
A;Cross-references: GB:M69296
A;Experimental source: clone 24; breast cancer
A;Note: sequence extracted from NCBI backbone (NCBIN:106597)
C;Comment: The steroid hormones and their receptors are involved in the regulation of eu
C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
complex appears to recognize discrete DNA sequences upstream of transcriptional start sit
C;Genetics:
A;C; GDB:ESR1; ESR
A;Cross-references: GDB:119120; OMIM:133430
A;Map position: 6q25.1-6q25.1
A;Introns: 151/2; 215/1; 254/1; 366/1; 412/2; 457/1; 518/2
C;Superfamily: estrogen receptor; erBA transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid hormone receptor; transcrip
F;1-120/Domain: amino-terminal <NH2>
F;121-299/Domain: DNA binding #status predicted <DNA>
F;183-456/Domain: erBA transforming protein homology <ERBA>
F;185-205/Region: zinc finger CCCC motif
F;221-245/Region: zinc finger CCCC motif
F;300-595/Domain: steroid binding #status predicted <STB>
F;236,305/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 98.4%; Score 1230.5; DB 1; Length 595;
Best Local Similarity 99.2%; Pred. No. 1.3e-98;
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 364

QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVEGMVEI 120
Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPVPLLAPNLLDRNQKCVEGMVEI 424

QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 425 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484

QY 180 TLIHLMKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKNVVPLYDLLLEML 239
Db 485 TLIHLMKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKNVVPLYDLLLEML 544

QY 240 DAHRL 244
Db 545 DAHRL 549

RESULT 2
QRMSE
estrogen receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: A40061
R;White, R.; Lees, J.A.; Needham, M.; Ham, J.; Parker, M.
Mol. Endocrinol. 1, 735-744, 1987
A;Title: Structural organization and expression of the mouse estrogen receptor.
A;Reference number: A40061; MUID:91042558; PMID:2484714
A;Accession: A40061
A;Molecule type: mRNA
A;Residues: 1-599 <WHI>
A;Cross-references: UNIPROT:P19785; GB:M38651; NID:g193179; PIDN:AAA37580.1; PID:g193180
C;Comment: The steroid hormones and their receptors are involved in the regulation of eu

C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
complex appears to recognize discrete DNA sequences upstream of transcriptional start sit
C;Superfamily: estrogen receptor; erBA transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recept
F;1-183/Domain: amino-terminal <NH2>
F;184-275/Domain: DNA binding #status predicted <DNA>
F;187-460/Domain: erBA transforming protein homology <ERBA>
F;187-210/Region: zinc finger CCCC motif
F;223-245/Region: zinc finger CCCC motif
F;260-275/Region: nuclear location signal
F;304-556/Domain: steroid binding #status predicted <STB>
F;189,192,206,209/Binding site: zinc (Cys) #status predicted
F;225,231,241,244/Binding site: zinc (Cys) #status predicted
F;240,309/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 96.4%; Score 1204.5; DB 1; Length 599;
Best Local Similarity 96.3%; Pred. No. 2.4e-96;
Matches 236; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 60
Db 309 SPALSLTADQMVSALLDAEPPMIYSEYDPSRPFPSEASMMGLLTNLADRELVHMINWAKRV 368

QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVEGMVEI 120
Db 369 PGFGDLNLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVEGMVEI 428

QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 429 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 488

QY 180 TLIHLMKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKNVVPLYDLLLEML 239
Db 489 TLIHLMKAGLTLQQHRRLAQLLLILSHIRHMSNKGMEHLYSMCKNVVPLYDLLLEML 548

QY 240 DAHRL 244
Db 549 DAHRL 553

RESULT 3
QRRTE
estrogen receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: S07379; S16731
R;Koike, S.; Sakai, M.; Muramatsu, M.
Nucleic Acids Res. 15, 2499-2513, 1987
A;Title: Molecular cloning and characterization of rat estrogen receptor cDNA.
A;Reference number: S07379; MUID:87174780; PMID:3031601
A;Accession: S07379
A;Molecule type: mRNA
A;Residues: 1-600 <KOI>
A;Cross-references: UNIPROT:P06211; EMBL:Y00102; NID:g56110; PIDN:CAA68287.1; PID:g56111
R;Maggi, A.M.A.
submitted to the EMBL Data Library, June 1991
A;Reference number: S16731
A;Accession: S16731
A;Molecule type: mRNA
A;Residues: 1-487,'T',489-600 <MAG>
A;Cross-references: EMBL:X61098; NID:g56120; PIDN:CAA43411.1; PID:g56121
C;Comment: The steroid hormones and their receptors are involved in the regulation of eu
C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
complex appears to recognize discrete DNA sequences upstream of transcriptional start sit
C;Superfamily: estrogen receptor; erBA transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recept
F;1-184/Domain: amino-terminal <NH2>
F;185-276/Domain: DNA binding #status predicted <DNA>
F;188-461/Domain: erBA transforming protein homology <ERBA>
F;188-211/Region: zinc finger CCCC motif
F;224-246/Region: zinc finger CCCC motif
F;261-276/Region: nuclear location signal
F;305-557/Domain: steroid binding #status predicted <STB>

F;236,305/Binding site: phosphate (Ser) (covalent) #status predicted

Db 605 QQHQRLAQLLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEMLDAHRL 655

RESULT 6

QRCHE
estrogen receptor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: A40914; S07192
R;Maxwell, B.L.; McDonnell, D.P.; Conneely, O.M.; Schulz, T.Z.; Greene, G.L.; O'Malley, M.L. Endocrinol. 1, 25-35, 1987
A;Title: Structural organization and regulation of the chicken estrogen receptor.
A;Reference number: A40914; MUID:88318621; PMID:2901032
A;Accession: A40914
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-589 <MAX>
A;Cross-references: UNIPROT:P06212
R;Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P. EMBO J. 5, 891-897, 1986
A;Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human oes
A;Reference number: S07192; MUID:86247578; PMID:3755102
A;Accession: S07192
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-256, 'E', 258-589 <KRU>
A;Cross-references: EMBL:X03805; NID:g63378; PIDN:CAA27433.1; PID:g63380
C;Comment: The steroid hormones and their receptors are involved in the regulation of eu
C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
complex appears to recognize discrete DNA sequences upstream of transcriptional start sit
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep
F;1-173/Domain: amino-terminal <NH2>
F;174-265/Domain: DNA binding #status predicted <DNA>
F;177-450/Domain: erba transforming protein homology <ERBA>
F;177-200/Region: zinc finger CCCC motif
F;213-235/Region: zinc finger CCCC motif
F;250-265/Region: nuclear location signal
F;294-546/Domain: steroid binding #status predicted <STB>
F;179,182,196,199/Binding site: zinc (Cys) #status predicted
F;215,221,231,234/Binding site: zinc (Cys) #status predicted
F;230,299/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 94.1%; Score 1176.5; DB 1; Length 589;
Best Local Similarity 93.5%; Pred. No. 6.2e-94;
Matches 229; Conservative 12; Mismatches 3; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSSEASMMGLLTNLADRELVHMINWAKRV 60
Db 299 SPALSLTAEQMVSAALLAEPPIVYSEYDPTNRPFSSEASMMGLLTNLADRELVHMINWAKRV 358

QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGEMVEI 120
Db 359 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGEMVEI 418

QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 419 FDMLLATAARFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEERDYIHRVLDKITD 478

QY 180 TLIHLMKAGLTLQQQHQRLLAQLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLLEML 239
Db 479 TLIHLMKAGLTLQQQHRRLLAQLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLLEML 538

QY 240 DAHRL 244
Db 539 DAHRL 543

RESULT 7

QRCHE
estrogen receptor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 28-Feb-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: A40907

R;Weiler, I.J.; Lew, D.; Shapiro, D.J. Mol. Endocrinol. 1, 355-362, 1987
A;Title: The Xenopus laevis estrogen receptor: sequence homology with human and avian rec
A;Reference number: A40907; MUID:90331927; PMID:3274894
A;Accession: A40907
A;Molecule type: mRNA
A;Residues: 1-586 <WEI>
A;Cross-references: UNIPROT:P81559; GB:L20735
C;Comment: The steroid hormones and their receptors are involved in the regulation of eu
C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
complex appears to recognize discrete DNA sequences upstream of transcriptional start site
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep
F;1-174/Domain: amino-terminal <NH2>
F;175-266/Domain: DNA binding #status predicted <DNA>
F;178-448/Domain: erba transforming protein homology <ERBA>
F;178-201/Region: zinc finger CCCC motif
F;214-237/Region: zinc finger CCCC motif
F;251-266/Region: nuclear location signal
F;292-544/Domain: steroid binding #status predicted <STB>
F;180,183,197,200/Binding site: zinc (Cys) #status predicted
F;216,222,232,235/Binding site: zinc (Cys) #status predicted
F;231/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 85.3%; Score 1066.5; DB 1; Length 586;
Best Local Similarity 82.9%; Pred. No. 2e-84;
Matches 203; Conservative 26; Mismatches 15; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSSEASMMGLLTNLADRELVHMINWAKRV 60
Db 297 SPVLSLTAEQLISALMEAEPIVSEHDSTKPLSEASMMTLLTNLADRELVHMINWAKRV 356

QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGEMVEI 120
Db 357 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLSFAPNLLDRNQRCVEGLVEI 416

QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 417 FDMLVTTATFRMRRLRGEFEFCLKSIILLNSGVYTFLSSTLESLEDTLHIILDKIID 476

QY 180 TLIHLMKAGLTLQQQHQRLLAQLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLLEML 239
Db 477 TLVHFMAKSGLSLQQQRRLLAQLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLLEML 536

QY 240 DAHRL 244
Db 537 DAHRI 541

RESULT 8

T10423
estrogen receptor - Oryzias sp. (strain d-rR)
C;Species: Oryzias sp.
A;Variety: strain d-rR
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T10423
R;Okada, H.; Kawahara, T.; Yamashita, I. submitted to the EMBL Data Library, March 1994
A;Description: Cloning of medaka estrogen receptor cDNA.
A;Reference number: Z17013
A;Accession: T10423
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-620 <OKA>
A;Cross-references: UNIPROT:P50241; EMBL:D28954
A;Experimental source: strain d-rR, liver
C;Genetics:
A;Gene: MER
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation
F;184-460/Domain: erba transforming protein homology <ERB>

Query Match 64.4%; Score 804.5; DB 2; Length 620;


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QY 5 SLTADQMVSALLDAEPP-ILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRVPGF 63
Db 209 ALSPEQLVLTLLAEPPHVLISR--PSAPFTEASMMMSLTKLADKELVHMISWAKKIPGF 266

QY 64 VDLTLHDQVHLLCAWLIELMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVEGMVEIFDM 123
Db 267 VELSLFDQVRLLESCWMEVLMGLMWSRIDHPGKLI FAPDLVDRDEGKCVEGILEIFDM 326

QY 124 LLATSSRRFRMMNLQ-GEFVCLKSIILLNSGVYTFSLSTLSLEEKDHIHRVLDKITDTLI 182
Db 327 LLATTSRRFRELKLQHKYLCVKAMILLNSSMYPPLVTAT-QDADSSRKLAAHLLNAVTDALV 385

QY 183 HLMKAGLTLLQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLLLLEMLDAH 242
Db 386 WVIKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMCKKNVVPVLYDLLLLLEMLNAH 445

QY 243 RL 244
Db 446 VL 447

RESULT 12
JC5939
estrogen receptor beta - human
C:Species: Homo sapiens (man)
C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C:Accession: JC5939
R:Ogawa, S.; Inoue, S.; Watanabe, T.; Hiroi, H.; Orimo, A.; Hosoi, T.; Ouchi, Y.; Muramatsu, T.
Biochem. Biophys. Res. Commun. 243, 122-126, 1998
A:Title: The complete primary structure of human estrogen receptor beta (hERbeta) and its
A:Reference number: JC5939; MUID:98139878; PMID:9473491
A:Accession: JC5939
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-530 <OGA>
A:Cross-references: DDBJ:AB006590; NID:G2911151; PIDN:BAA24953.1; PID:G2911152
C:Superfamily: estrogen receptor; erbA transforming protein homology
F:147-408/Domain: erbA transforming protein homology <ERB>

Query Match 60.8%; Score 759.5; DB 2; Length 530;
Best Local Similarity 59.5%; Pred. No. 6.5e-58;
Matches 144; Conservative 56; Mismatches 37; Indels 5; Gaps 4;

QY 5 SLTADQMVSALLDAEPP-ILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRVPGF 63
Db 262 ALSPEQLVLTLLAEPPHVLISR--PSAPFTEASMMMSLTKLADKELVHMISWAKKIPGF 319

QY 64 VDLTLHDQVHLLCAWLIELMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVEGMVEIFDM 123
Db 320 VELSLFDQVRLLESCWMEVLMGLMWSRIDHPGKLI FAPDLVDRDEGKCVEGILEIFDM 379

QY 124 LLATSSRRFRMMNLQ-GEFVCLKSIILLNSGVYTFSLSTLSLEEKDHIHRVLDKITDTLI 182
Db 380 LLATTSRRFRELKLQHKYLCVKAMILLNSSMYPPLVTAT-QDADSSRKLAAHLLNAVTDALV 438

QY 183 HLMKAGLTLLQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLLLLEMLDAH 242
Db 439 WVIKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMCKKNVVPVLYDLLLLLEMLNAH 498

QY 243 RL 244
Db 499 VL 500

RESULT 13
JW0046
estrogen receptor beta2 - rat
N:Alternate names: ERbeta2
C:Species: Rattus norvegicus (Norway rat)
C>Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 17-Mar-1999
C:Accession: JW0046
R:Maruyama, K.; Endoh, H.; Sasaki-Iwaoka, H.; Kanou, H.; Shimaya, E.; Hashimoto, S.; Kato, T.
Biochem. Biophys. Res. Commun. 246, 142-147, 1998

```

C;Species: Macaca mulatta (rhesus macaque)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C;Accession: I67419
R;Chandrasekhar, Y.A.; Melner, M.H.; Nagalla, S.R.; Stouffer, R.L.
Endocrinology 135, 307-314, 1994
A;Title: Progesterone receptor, but not estradiol receptor, messenger ribonucleic acid
A;Reference number: I53287; MUID:94283272; PMID:8013365
A;Accession: I67419
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-121 <RES>
A;Cross-references: UNIPROT:P49886; GB:S71040; NID:G547182; PIDN:AAB31102.1; PID:G547183
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: steroid hormone receptor; zinc finger
F;1-54/Domain: erba transforming protein homology (fragment) <ERBA>

Query Match	46.4%	Score	580.5;	DB	2;	Length	121;
Best Local Similarity	97.5%	Pred. No.	3.2e-43;				
Matches	118;	Conservative	1;	Mismatches	1;	Indels	1;
		Gaps	1;				
Qy	99	LFAPNLLLDNRNQKCV	EGMVEIFDMLLATSSRFRMNLQ	GFVCLKSIILLNSGVYTF	L	157	
Db	1	LFAPNLLLDNRNQKCV	EGMVEISFDMLLATSSRFRMNLQ	GFVCLKSIILLNSGVYTF	L	60	
Qy	158	SSTLKSLEEKDHIHRV	LDKITDTLIHLMAKAGLT	LQQQHQR	LQALLLILSHIRHMSNKG	M	217
Db	61	SSTLKSLEEKDHIHRV	LDKITDTLIHLMAKAGLT	LQQQHRR	LQALLLILSHIRHMSNKG	M	120
Qy	218	E	218				
Db	121	E	121				

Search completed: November 8, 2004, 08:28:28
Job time : 12.951 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 8, 2004, 08:28:04 ; Search time 36.849 Seconds
(without alignments)
2338.928 Million cell updates/sec

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Perfect score: 1250
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues
Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA: *
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1239.5	99.2	414	14	US-10-157-899A-2
2	1239.5	99.2	438	14	US-10-157-899A-4
3	1239.5	99.2	595	9	US-09-853-033-2
4	1239.5	99.2	595	14	US-10-148-835-1
5	1239.5	99.2	595	14	US-10-148-835-2
6	1239.5	99.2	595	14	US-10-148-835-9
7	1235.5	98.8	595	14	US-10-148-835-5
8	1233.5	98.7	595	14	US-10-148-835-3
9	1232.5	98.6	595	14	US-10-148-835-4
10	1232.5	98.6	595	14	US-10-148-835-10
11	1231.5	98.5	595	14	US-10-148-835-8
12	1231.5	98.5	660	9	US-09-853-033-4
13	1230.5	98.4	414	14	US-10-157-899A-8

14	1230.5	98.4	438	14	US-10-157-899A-14
15	1230.5	98.4	511	14	US-10-006-760-19
16	1230.5	98.4	547	14	US-10-052-092-10
17	1230.5	98.4	547	14	US-10-437-107-10
18	1230.5	98.4	591	14	US-10-278-481-17
19	1230.5	98.4	595	9	US-09-933-267A-2
20	1230.5	98.4	595	10	US-09-952-680A-10
21	1230.5	98.4	595	13	US-10-096-710-1
22	1230.5	98.4	595	13	US-10-081-563-2
23	1230.5	98.4	595	14	US-10-052-092-9
24	1230.5	98.4	595	14	US-10-052-092-13
25	1230.5	98.4	595	14	US-10-052-092-14
26	1230.5	98.4	595	14	US-10-207-655-61
27	1230.5	98.4	595	14	US-10-177-293-128
28	1230.5	98.4	595	14	US-10-157-899A-55
29	1230.5	98.4	595	14	US-10-437-107-9
30	1230.5	98.4	595	14	US-10-437-107-13
31	1230.5	98.4	595	14	US-10-437-107-14
32	1230.5	98.4	595	14	US-10-095-373A-2
33	1230.5	98.4	595	14	US-10-392-274-2
34	1230.5	98.4	595	14	US-10-148-835-6
35	1230.5	98.4	595	14	US-10-148-835-7
36	1230.5	98.4	595	14	US-10-144-198-42
37	1230.5	98.4	676	14	US-10-095-373A-73
38	1230.5	98.4	677	14	US-10-095-373A-69
39	1230.5	98.4	726	14	US-10-095-373A-71
40	1230.5	98.4	727	14	US-10-095-373A-67
41	1229.5	98.4	414	14	US-10-157-899A-10
42	1229.5	98.4	438	14	US-10-157-899A-16
43	1228.5	98.3	660	9	US-09-853-033-8
44	1227.5	98.2	242	15	US-10-355-218-10
45	1225.5	98.0	414	14	US-10-157-899A-6

ALIGNMENTS

RESULT 1

US-10-157-899A-2
; Sequence 2, Application US/10157899A
; Publication No. US20030143559A1
; GENERAL INFORMATION:
; APPLICANT: Bracken, Kathryn Rene
; APPLICANT: de los Angeles, Joseph Ernest
; APPLICANT: Huang, Ying
; APPLICANT: Kadan, Michael Joseph
; APPLICANT: Ksander, Gary Michael
; APPLICANT: Zerby, Dennis
; TITLE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL
; FILE REFERENCE: 4-32018A
; CURRENT APPLICATION NUMBER: US/10/157,899A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/294,839
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion of the human-estrogen-receptor-ligand-binding-domain and a
; OTHER INFORMATION: zinc finger array(C7)
US-10-157-899A-2

Query Match 99.2%; Score 1239.5; DB 14; Length 414;
Best Local Similarity 99.6%; Pred. No. 2e-118;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFFSEASMMGLLTNLADRELVHMINKRV 60
Db 122 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFFSEASMMGLLTNLADRELVHMINKRV 181

Qy	61	PGFVDLT	LHDQVHLL	ECAWLEI	IMIGLVW	RSMHPGK	LLFAPNLLL	DRNQKCVEGM	VEI	120
Dd	182	PGFVDLT	LHDQVHLL	ECAWLEI	IMIGLVW	RSMHPGK	LLFAPNLLL	DRNQKCVEGM	VEI	241
Qy	121	FDMLLAT	SSTRFRM	NLQG-EF	VCLKSI	ILLNSGVY	TFLSSTLK	SLEEKDHIHRVL	DKITD	179
Dd	242	FDMLLAT	SSTRFRM	NLQGEF	VCLKSI	ILLNSGVY	TFLSSTLK	SLEEKDHIHRVL	DKITD	301
Qy	180	TLIHLMA	KAGLT	LQQQHQR	LAQLLL	ILSHIRH	MNSKGMEHLY	SMCKCNVVPLYD	LLLEML	239
Dd	302	TLIHLMA	KAGLT	LQQQHQR	LAQLLL	ILSHIRH	MNSKGMEHLY	SMCKCNVVPLYD	LLLEML	361
Qy	240	DAHRL	244							
Dd	362	DAHRL	366							

RESULT 2
US-157-899A-4
Sequence 4, Application US/10157899A
Publication No. US20030143559A1
GENERAL INFORMATION:
APPLICANT: Bracken, Kathryn Rene
APPLICANT: de los Angeles, Joseph Ernest
APPLICANT: Huang, Ying
APPLICANT: Kadan, Michael Joseph
APPLICANT: Ksander, Gary Michael
APPLICANT: Zerby, Dennis
TITLE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL
TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS
FILE REFERENCE: 4-32018A
CURRENT APPLICATION NUMBER: US/10/157,899A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/294,839
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 438
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion of the human-Estrogen-receptor-ligand-binding-domain and
US-10-157-899A-4

RESULT 3

US-09-853-033-2
; Sequence 2, Application US/09853033
; Patent No. US20020100068A1
; GENERAL INFORMATION:
; APPLICANT: CHAMBON, PIERRE
; APPLICANT: METZGER, DANIEL
; TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
; TITLE OF INVENTION: MEDIATED BY MODIFIED CRE-ER
; FILE REFERENCE: 065691/0222
; CURRENT APPLICATION NUMBER: US/09/853,033
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: FR 00/12570
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-033-2

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RESULT 4
US-10-148-835-1
; Sequence 1, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-1

```

QY 61 PGFVDLTLDHDOVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCEGMVEI 120

Db 365 PGFVDLTLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 424
Qy 121 FDMLLATSSRRFRMMNLQ- EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 425 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484
Qy 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 239
Db 485 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 544
Qy 240 DAHRL 244
Db 545 DAHRL 549

RESULT 5
US-10-148-835-2
; Sequence 2, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-2

Query Match 99.2%; Score 1239.5; DB 14; Length 595;
Best Local Similarity 99.6%; Pred. No. 3.2e-118;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 SLALSLTADQMVSALLDAEPPILYSEYDPTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSALLDAEPPILYSEYDPTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
Qy 61 PGFVDLTLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120
Db 365 PGFVDLTLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 424
Qy 121 FDMLLATSSRRFRMMNLQ- EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 425 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484
Qy 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 239
Db 485 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 544
Qy 240 DAHRL 244
Db 545 DAHRL 549

RESULT 6
US-10-148-835-9
; Sequence 9, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 595

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-9
Query Match 99.2%; Score 1239.5; DB 14; Length 595;
Best Local Similarity 99.6%; Pred. No. 3.2e-118;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 SLALSLTADQMVSALLDAEPPILYSEYDPTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSALLDAEPPILYSEYDPTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
Qy 61 PGFVDLTLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120
Db 365 PGFVDLTLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 424
Qy 121 FDMLLATSSRRFRMMNLQ- EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 425 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484
Qy 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 239
Db 485 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 544
Qy 240 DAHRL 244
Db 545 DAHRL 549

RESULT 7
US-10-148-835-5
; Sequence 5, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-5

Query Match 98.8%; Score 1235.5; DB 14; Length 595;
Best Local Similarity 99.2%; Pred. No. 8.3e-118;
Matches 243; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Qy 1 SLALSLTADQMVSALLDAEPPILYSEYDPTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSALLDAEPPILYSEYDPTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
Qy 61 PGFVDLTLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120
Db 365 PGFVDLTLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 424
Qy 121 FDMLLATSSRRFRMMNLQ- EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 425 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484
Qy 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 239
Db 485 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 544
Qy 240 DAHRL 244
Db 545 DAHRL 549

RESULT 8

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US-10-148-835-3
; Sequence 3, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-3

Query Match      98.7%; Score 1233.5; DB 14; Length 595;
Best Local Similarity 99.2%; Pred. No. 1.3e-117;
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY      1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 60
      |||||
Db      305 SLALFLTADQMVSAALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 364

QY      61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEI 120
      |||||
Db      365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEI 424

QY      121 FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
      |||||
Db      425 FDMLLATSSRFRMMNLQGEFEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484

QY      180 TLIHLMKAGLTQQQHQRLAQLLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 239
      |||||
Db      485 TLIHLMKAGLTQQQHQRLAQLLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 544

QY      240 DAHRL 244
      |||||
Db      545 DAHRL 549

RESULT 9
US-10-148-835-4
; Sequence 4, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-4

Query Match      98.6%; Score 1232.5; DB 14; Length 595;
Best Local Similarity 99.2%; Pred. No. 1.7e-117;
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY      1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 60
      |||||
Db      305 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 364

QY      61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEI 120
      |||||
Db      365 PGFVDLTLDQVHLLLECAWLEILMIDLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEI 424

QY      121 FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
      |||||
Db      425 FDMLLATSSRFRMMNLQGEFEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484

QY      180 TLIHLMKAGLTQQQHQRLAQLLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 239
      |||||
Db      485 TLIHLMKAGLTQQQHQRLAQLLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 544

QY      240 DAHRL 244
      |||||
Db      545 DAHRL 549

RESULT 11
US-10-148-835-8
; Sequence 8, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-8

Query Match      98.6%; Score 1232.5; DB 14; Length 595;
Best Local Similarity 99.2%; Pred. No. 1.7e-117;
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY      1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 60
      |||||
Db      305 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 364

QY      61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEI 120
      |||||
Db      365 PGFVDLTLDQVHLLLECAWLEILMIDLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEI 424

QY      121 FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
      |||||
Db      425 FDMLLATSSRFRMMNLQGEFEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484

QY      180 TLIHLMKAGLTQQQHQRLAQLLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 239
      |||||
Db      485 TLIHLMKAGLTQQQHQRLAQLLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 544

QY      240 DAHRL 244
      |||||
Db      545 DAHRL 549
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Query Match	98.5%;	Score 1231.5;	DB 14;	Length 595;			
Best Local Similarity	98.8%;	Pred. No. 2.1e-117;					
Matches 242;	Conservative	2;	Mismatches	0;			
			Indels	1;			
			Gaps	1;			
QY	1	SLALSLTADQMV	SALLDAEPPPILYSEYDPT	TRPFSEASMMGLLTNLADREL	VHMINWAKRV	60	
DB	305	SLALSLTADQMV	SALLDAEPPPILYSEYDPT	TRPFSEASMMGLLTNLADREL	VHMINWAKRV	364	
QY	61	PGFVDLTLDH	QVHLLCEAWLEILMIGLV	WRSMHPGKLLFAPNLL	LDNRQKCV	EGMVEI 120	
DB	365	PGFVDLTLDH	QVHLLCEAWLEILMIGLV	WRSMHPGKLLFAPNLL	LDNRQKCV	EGMVEI 424	
QY	121	FDMLLATSSR	FRMMNLQG-EFVCLKSI	ILLNSGVYTFISSTLKS	LEEKDH	IHRVLDKITD 179	
DB	425	FDMLLATSSR	FRMMNLQGEFVCLKSI	ILLNSGVYTFISSTLKS	LEEKDH	IHRVLDKITD 484	
QY	180	TLIHLMAKAGL	TLQQQHQR	LAQLLLILSHIRHMS	KNKGHEHLY	SMCKKNVVP	LYDLLLEML 239
DB	485	TLIHLMAKAGL	TLQQQHQR	LAQLLLILSHIRHMS	KNKGHEHLY	SMCKKNVVP	LYDLLLEML 544
QY	240	DAHRL	244				
DB	545	DAHRL	549				

```

RESULT 12
US-09-853-033-4
; Sequence 4, Application US/09853033
; Patent No. US20020100068A1
; GENERAL INFORMATION:
; APPLICANT: CHAMBON, PIERRE
; APPLICANT: METZGER, DANIEL
; TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
; TITLE OF INVENTION: MEDIATED BY MODIFIED CRE-ER
; FILE REFERENCE: 065691/0222
; CURRENT APPLICATION NUMBER: US/09/853,033
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: FR 00/12570
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 660
; TYPE: prt
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric sequence
; OTHER INFORMATION: Homosapiens-Bacteriophage P1
US-09-853-033-4

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Query Match	98.5%	Score 1231.5;	DB 9;	Length 660;
Best Local Similarity	99.2%	Pred. No. 2.5e-117;		
Matches 243;	Conservative 0;	Mismatches 1;	Indels 1;	Gaps 1;
Qy 1	SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV	60		
Db 370	SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV	429		
Qy 61	PGFVDLTILHDQVHLLIECAWLLEILMIGLVWRSMHPGKLLFAPNLLLDNRNQKCVGEMVEI	120		
Db 430	PGFVDLTILHDQVHLLIECAWLLEILMIGLVWRSMHPGKLLFAPNLLLDNRNQKCVGEMVEI	489		
Qy 121	FDMLLATSSRFRRMNLQG-EFVCLKSIIILNSGVYTFLSSTLKSLEEKDHIHRVLDKITD	179		
Db 490	FDMLLATSSRFRRMNLQGEFVCLKSIIILNSGVYTFLSSTLKSLEEKDHIHRVLDKITD	549		
Qy 180	TLIHLMAKAGLTLOQHQHRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPPLYDLLEML	239		
Db 550	TLIHLMAKAGLTLOQHQHRLAQLLLILSHIRHMSNKRMEHLYSMCKKNVVPPLYDLLEML	609		
Qy 240	DAHRL	244		
Db 610	DAHRL	614		

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RESULT 13
US-10-157-899A-8
; Sequence 8, Application US/10157899A
; Publication No. US20030143559A1
; GENERAL INFORMATION:
; APPLICANT: Bracken, Kathryn Rene
; APPLICANT: de los Angeles, Joseph Ernest
; APPLICANT: Huang, Ying
; APPLICANT: Kadan, Michael Joseph
; APPLICANT: Ksander, Gary Michael
; APPLICANT: Zerby, Dennis
; TITLE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL
; TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 4-32018A
; CURRENT APPLICATION NUMBER: US/10/157,899A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/294,839
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion of a mutated human-Estrogen-receptor-ligand-binding-domain
; OTHER INFORMATION: and a zinc finger array (C7)
US-10-157-899A-8

```

Query Match 98.4%; Score 1230.5; DB 14; Length 414;
Best Local Similarity 98.8%; Pred. No. 1.7e-117;
Matches 242; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY	1	SLALSLTADQMV	SALLDAEPPILYSEYDPT	RPFSEASMMGLLTNLADREL	VHMINWAKRV	60
Db	122	SLALSLTADQMV	SALLDAEPPILYSEYDPT	RPFSEASMMGLLTNLADREL	VHMINWAKRV	181
QY	61	PGFVDLTLDQV	HLLECAWLEILMIGLVWRS	MEHPGKLLFAPNLLDRNQ	KCVEGMVEI	120
Db	182	PGFVDLTLDQV	HLLECAWLEILMIGLVWRS	MEHPGKLLFAPNLLDRNQ	KCVEGMVEI	241
QY	121	FDMLLATSSR	FRMMNLQGEFVCLKSI	ILLNSGVYTFLSSTLS	EKDHHRVLDKITD	179
Db	242	FDMLLATSSR	FRMMNLQGEFVCLKSI	ILLNSGVYTFLSSTLS	EKDHHRVLDKITD	301
QY	180	TLIHLMAKAGL	TQQQHQR	LAQLLLILSHIRHMSN	KGMHELYSMKCKNVVPLYD	LLLEML 239
Db	302	TLIHLMAKAGL	TQQQHQR	LAQLLLILSHIRHMSN	KGMHELYSMKCKNVVPLYD	LLLEML 361
QY	240	DAHRL	244			
Db	362	DAHRL	366			

RESULT 14
US-10-157-899A-14
; Sequence 14, Application US/10157899A
; Publication No. US20030143559A1
; GENERAL INFORMATION:
; APPLICANT: Bracken, Kathryn Rene
; APPLICANT: de los Angeles, Joseph Ernest
; APPLICANT: Huang, Ying
; APPLICANT: Kadan, Michael Joseph
; APPLICANT: Ksander, Gary Michael
; APPLICANT: Zerby, Dennis
; TITLE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL
; TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 4-32018A
; CURRENT APPLICATION NUMBER: US/10/157,899A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/294,839

; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion of a mutated human-Estrogen-receptor-ligand-binding-domain
; OTHER INFORMATION: and a zinc finger array(C7)
US-10-157-899A-14

Query Match 98.4%; Score 1230.5; DB 14; Length 438;
Best Local Similarity 98.8%; Pred. No. 1.8e-117;
Matches 242; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 60
Db 146 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 205
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVGEMVEI 120
Db 206 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVGEMVEI 265
QY 121 FDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 266 FDMALATSSRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 325
QY 180 TLIHLMKAGLTLQQQHQRLAQLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEML 239
Db 326 TLIHLMKAGLTLQQQHQRLAQLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEML 385
QY 240 DAHRL 244
Db 386 DAHRL 390

RESULT 15
US-10-006-760-19
; Sequence 19, Application US/10006760
; Publication No. US20030186385A1
; GENERAL INFORMATION:
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBOODIES WHICH BIND
; TITLE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF
; FILE REFERENCE: 176/60901
; CURRENT APPLICATION NUMBER: US/10/006,760
; CURRENT FILING DATE: 2001-11-19
; OR APPLICATION NUMBER: 60/249,756
; OR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: lexA-ER(alpha)EF fusion protein
US-10-006-760-19

Query Match 98.4%; Score 1230.5; DB 14; Length 511;
Best Local Similarity 99.2%; Pred. No. 2.2e-117;
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 60
Db 221 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 280
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVGEMVEI 120
Db 281 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPVKLLFAPNLLLDNRNQGKCVGEMVEI 340

QY 121 FDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 341 FDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 400
QY 180 TLIHLMKAGLTLQQQHQRLAQLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEML 239
Db 401 TLIHLMKAGLTLQQQHQRLAQLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEML 460
QY 240 DAHRL 244
Db 461 DAHRL 465

Search completed: November 8, 2004, 08:42:49
Job time : 37.849 secs

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OM protein - protein search, using sw model

Run on: November 8, 2004, 08:16:47 ; Search time 14.4408 Seconds
(without alignments)
1120.546 Million cell updates/sec

Title: US-09-830-693B-27
Perfect score: 1250
Sequence: 1 SLALSLTADQMVSALLDAEP.....CKNVVPLYDLLLEMLDAHRL 244

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Sequences: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCFUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1239.5	99.2	595	3	US-08-764-870-12
2	1239.5	99.2	595	3	US-08-980-115-12
3	1230.5	98.4	591	2	US-08-836-620A-17
4	1230.5	98.4	595	3	US-09-041-886-35
5	1230.5	98.4	595	4	US-08-453-998-2
6	1230.5	98.4	651	3	US-08-693-940-3
7	1230.5	98.4	651	3	US-09-566-660-3
8	1230.5	98.4	773	3	US-08-564-264-1
9	1213	97.0	410	6	5223606-5
10	1200.5	96.0	596	2	US-08-836-620A-16
11	1179	94.3	264	4	US-09-660-979-1
12	994.5	79.6	243	2	US-08-836-620A-10
13	984.5	78.8	243	2	US-08-836-620A-9
14	979.5	78.4	243	2	US-08-836-620A-8
15	804.5	64.4	575	4	US-09-893-666A-2
16	765.5	61.2	484	2	US-08-836-620A-13
17	765.5	61.2	485	2	US-08-836-620A-2
18	759.5	60.8	477	4	US-09-608-088-5
19	759.5	60.8	477	4	US-09-711-288-5
20	759.5	60.8	485	2	US-08-836-620A-3
21	759.5	60.8	530	4	US-09-608-088-25
22	759.5	60.8	530	4	US-09-711-288-25
23	759.5	60.8	548	3	US-09-139-617-1
24	759.5	60.8	548	4	US-09-561-741A-1
25	759.5	60.8	548	4	US-09-558-795-1
26	751.5	60.1	484	2	US-08-836-620A-14
27	751.5	60.1	485	2	US-08-836-620A-5

28	747.5	59.8	233	4	US-09-608-088-4	Sequence 4, Appli
29	747.5	59.8	233	4	US-09-711-288-4	Sequence 4, Appli
30	730	58.4	229	3	US-09-249-645-1	Sequence 1, Appli
31	726	58.1	229	4	US-09-844-132B-1	Sequence 1, Appli
32	696.5	55.7	228	3	US-09-249-645-2	Sequence 2, Appli
33	696.5	55.7	228	4	US-09-844-132B-2	Sequence 2, Appli
34	663	53.0	226	2	US-08-836-620A-7	Sequence 7, Appli
35	618.5	49.5	384	2	US-08-836-620A-15	Sequence 15, Appli
36	618.5	49.5	416	4	US-09-608-088-6	Sequence 6, Appli
37	618.5	49.5	416	4	US-09-711-288-6	Sequence 6, Appli
38	618.5	49.5	418	4	US-09-608-088-21	Sequence 21, Appli
39	618.5	49.5	418	4	US-09-711-288-21	Sequence 21, Appli
40	514	41.1	97	4	US-09-652-345-5	Sequence 5, Appli
41	370.5	29.6	435	3	US-09-040-508-2	Sequence 2, Appli
42	370.5	29.6	435	3	US-09-500-654-2	Sequence 2, Appli
43	370.5	29.6	458	3	US-09-141-000-4	Sequence 4, Appli
44	368.5	29.5	431	2	US-08-836-620A-19	Sequence 19, Appli
45	364.5	29.2	500	3	US-09-141-000-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-764-870-12
; Sequence 12, Application US/08764870
; Patent No. 6236946
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Thomas S
; APPLICANT: Baxter, John D
; APPLICANT: Fletcher, Robert J
; APPLICANT: Wagner, Richard L
; APPLICANT: Kushner, Peter J
; APPLICANT: Apriletti, James W
; APPLICANT: West, Brian
; TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand
; TITLE OF INVENTION: Binding Domains
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,870
; FILING DATE: 13-DEC-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/008,540
; FILING DATE: 13-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/008,543
; FILING DATE: 13-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/008,606
; FILING DATE: 14-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: UCAL-246/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)843-5000
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 595 amino acids
; TYPE: amino acid

QY 180 TLHLMAKAGLTQQQHQRLAQQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLLEML 239
Db
QY 485 TLHLMAKAGLTQQQHQRLAQQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLLEML 544
QY 240 DAHRL 244
Db 545 DAHRL 549

RESULT 4
US-09-041-886-35
; Sequence 35, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 595 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-041-886-35

Query Match 98.4%; Score 1230.5; DB 3; Length 595;
Best Local Similarity 99.2%; Pred. No. 4.4e-124;
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFFSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVGEMVEI 120
Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPVKKLLFAPNLLLDNRNQGKCVGEMVEI 424
QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 425 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484
QY 180 TLHLMAKAGLTQQQHQRLAQQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLLEML 239
Db 485 TLHLMAKAGLTQQQHQRLAQQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLLEML 544
QY 240 DAHRL 244
|||||

Db 545 DAHRL 549
RESULT 5
US-08-453-998-2
; Sequence 2, Application US/08453998
; Patent No. 6444438
; GENERAL INFORMATION:
; APPLICANT: CHAMBER, PIERRE
; APPLICANT: METZGER, DANIEL
; APPLICANT: WHITE, JOHN
; TITLE OF INVENTION: METHOD FOR THE PREPARATION OF A PROTEIN
; TITLE OF INVENTION: BY YEASTS USING AN INDUCIBLE SYSTEM, VECTORS AND
; TITLE OF INVENTION: CORRESPONDING TRANSFORMED STRAINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVE., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,998
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/161,064
; FILING DATE: 03-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAPIN, MARLANA K.
; REGISTRATION NUMBER: 35,843
; REFERENCE/DOCKET NUMBER: 1037/98493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 595 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-453-998-2

Query Match 98.4%; Score 1230.5; DB 4; Length 595;
Best Local Similarity 99.2%; Pred. No. 4.4e-124;
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFFSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVGEMVEI 120
Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPVKKLLFAPNLLLDNRNQGKCVGEMVEI 424
QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 425 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484
QY 180 TLHLMAKAGLTQQQHQRLAQQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLLEML 239
Db 485 TLHLMAKAGLTQQQHQRLAQQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLLEML 544
QY 240 DAHRL 244
|||||

Db 545 DAHRL 549

RESULT 6

US-08-693-940-3

; Sequence 3, Application US/08693940

; Patent No. 6133027

; GENERAL INFORMATION:

; APPLICANT: Yee, Jiing-Kuan

; APPLICANT: Friedman, Theodore

; APPLICANT: Chen, Shin-Tai

; TITLE OF INVENTION: Inducible Expression System

; TITLE OF INVENTION: Useful in the Generation of packaging Cell Lines for

; TITLE OF INVENTION: Pseudotyped Retroviral Vectors

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bozicevic & Reed, LLP

; STREET: 285 Hamilton Ave, Suite 200

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/693,940

; FILING DATE: 07-AUG-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Francis, Carol L

; REGISTRATION NUMBER: 36,513

; REFERENCE/DOCKET NUMBER: 6510-055001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-327-3400

; TELEFAX: 650-327-3231

; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 651 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; AGENT TYPE: internal

US-08-693-940-3

Query Match 98.4%; Score 1230.5; DB 3; Length 651;

Best Local Similarity 99.2%; Pred. No. 5e-124;

Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 SLALSITADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 60

Db 361 SLALSITADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 420

QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPVKLLFAPNLLLDNRNQGKCVGMEVEI 120

Db 421 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPVKLLFAPNLLLDNRNQGKCVGMEVEI 480

QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHHRVLDKITD 179

Db 481 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHHRVLDKITD 540

QY 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEML 239

Db 541 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEML 600

QY 240 DAHRL 244

Db 240 DAHRL 605

RESULT 7

US-09-566-660-3

; Sequence 3, Application US/09566660

; Patent No. 6432705

; GENERAL INFORMATION:

; APPLICANT: Yee, Jiing-Kuan

; APPLICANT: Friedman, Theodore

; APPLICANT: Chen, Shin-Tai

; TITLE OF INVENTION: Inducible Expression System

; FILE REFERENCE: 6510-055CON

; CURRENT APPLICATION NUMBER: US/09/566,660

; CURRENT FILING DATE: 2000-05-08

; PRIOR APPLICATION NUMBER: 08/693,940

; PRIOR FILING DATE: 1996-08-07

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 651

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Multi-chimeric transactivating factor

US-09-566-660-3

Query Match 98.4%; Score 1230.5; DB 4; Length 651;

Best Local Similarity 99.2%; Pred. No. 5e-124;

Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 SLALSITADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 60

Db 361 SLALSITADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 420

QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPVKLLFAPNLLLDNRNQGKCVGMEVEI 120

Db 421 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPVKLLFAPNLLLDNRNQGKCVGMEVEI 480

QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHHRVLDKITD 179

Db 481 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHHRVLDKITD 540

QY 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEML 239

Db 541 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEML 600

QY 240 DAHRL 244

Db 601 DAHRL 605

RESULT 8

US-08-564-264-1

; Sequence 1, Application US/08564264

; Patent No. 6040430

; GENERAL INFORMATION:

; APPLICANT: STEWART, Francis

; TITLE OF INVENTION: REGULATION OF SITE-SPECIFIC

; TITLE OF INVENTION: RECOMBINATION BY SITE-SPECIFIC RECOMBINASE/NUCLEAR

; TITLE OF INVENTION: RECEPTOR FUSION PROTEINS

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram

; STREET: 655 Fifteenth Street N.W. Suite 330

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005-5701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

Db 601 DAHRL 605

RESULT 7

US-09-566-660-3

; Sequence 3, Application US/09566660

; Patent No. 6432705

; GENERAL INFORMATION:

; APPLICANT: Yee, Jiing-Kuan

; APPLICANT: Friedman, Theodore

; APPLICANT: Chen, Shin-Tai

; TITLE OF INVENTION: Inducible Expression System

; FILE REFERENCE: 6510-055CON

; CURRENT APPLICATION NUMBER: US/09/566,660

; CURRENT FILING DATE: 2000-05-08

; PRIOR APPLICATION NUMBER: 08/693,940

; PRIOR FILING DATE: 1996-08-07

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 651

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Multi-chimeric transactivating factor

US-09-566-660-3

Query Match 98.4%; Score 1230.5; DB 4; Length 651;

Best Local Similarity 99.2%; Pred. No. 5e-124;

Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 SLALSITADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 60

Db 361 SLALSITADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 420

QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPVKLLFAPNLLLDNRNQGKCVGMEVEI 120

Db 421 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPVKLLFAPNLLLDNRNQGKCVGMEVEI 480

QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHHRVLDKITD 179

Db 481 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHHRVLDKITD 540

QY 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEML 239

Db 541 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEML 600

QY 240 DAHRL 244

Db 601 DAHRL 605

RESULT 8

US-08-564-264-1

; Sequence 1, Application US/08564264

; Patent No. 6040430

; GENERAL INFORMATION:

; APPLICANT: STEWART, Francis

; TITLE OF INVENTION: REGULATION OF SITE-SPECIFIC

; TITLE OF INVENTION: RECOMBINATION BY SITE-SPECIFIC RECOMBINASE/NUCLEAR

; TITLE OF INVENTION: RECEPTOR FUSION PROTEINS

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram

; STREET: 655 Fifteenth Street N.W. Suite 330

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005-5701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,264
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02088
FILING DATE: 28-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 110 298.2
FILING DATE: 28-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Murray, Robert B.
REGISTRATION NUMBER: 22,980
REFERENCE/DOCKET NUMBER: P564-5019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 773 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc feature
LOCATION: (1-423)
OTHER INFORMATION: /note= "FLP recombinase domain."
FEATURE:
NAME/KEY: misc feature
LOCATION: (424-428)
OTHER INFORMATION: /note= "Linker peptide."
FEATURE:
NAME/KEY: misc feature
LOCATION: (429-773)
OTHER INFORMATION: /note= "Estrogen binding domain."
US-08-564-264-1

Query Match 98.4%; Score 1230.5; DB 3; Length 773;
Best Local Similarity 99.2%; Pred. No. 6.4e-124;
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTFPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 483 SLALSLTADQMVSAALLDAEPPILYSEYDPTFPFSEASMMGLLTNLADRELVHMINWAKRV 542
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120
Db 543 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 602
QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 603 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 662
QY 180 TLIHLMKAGLTQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLEML 239
Db 663 TLIHLMKAGLTQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLEML 722
QY 240 DAHRL 244
Db 723 DAHRL 727

RESULT 9
5223606-5
Patent No. 5223606
APPLICANT: BLAUDIN DE THE, HUGHES;MARCHIO, AGNES;TIOILLAIS,
PIERRE;DEJEAN, ANNE
TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED
PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/134,130
FILING DATE: 17-DEC-1987
PRIOR APPLICATION DATA:
SEQ ID NO:5:
LENGTH: 410
5223606-5
Query Match 97.0%; Score 1213; DB 6; Length 410;
Best Local Similarity 98.8%; Pred. No. 2e-122;
Matches 242; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTFPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 121 SLALSLTADQMVSAALLDAEPPILYSEYDPTFPFSEASMMGLLTNLADRELVHMINWAKRV 179
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120
Db 180 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 239
QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 240 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 299
QY 180 TLIHLMKAGLTQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLEML 239
Db 300 TLIHLMKAGLTQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLEML 359
QY 240 DAHRL 244
Db 360 DAHRL 364
RESULT 10
US-08-836-620A-16
Sequence 16, Application US/08836620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Rattus rattus
US-08-836-620A-16
Query Match 96.0%; Score 1200.5; DB 2; Length 596;
Best Local Similarity 95.9%; Pred. No. 7.7e-121;

[illegible]

```

RESULT 11
US-09-660-979-1
; Sequence 1, Application US/09660979
; Patent No. 6500629
; GENERAL INFORMATION:
; APPLICANT: Cleaver, Brian
; APPLICANT: Green, Mike L.
; TITLE OF INVENTION: Materials and Methods for Detection and Quantitation of an Analy
; FILE REFERENCE: ELI-101XC1
; CURRENT APPLICATION NUMBER: US/09/660,979
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,627
; PRIOR FILING DATE: 1999-09-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Equus
US-09-660-979-1

```

Query Match	94.3%;	Score 1179;	DB 4;	Length 264;
Best Local Similarity	94.7%;	Pred. No. 5.1e-119;		
Matches 232;	Conservative	7;	Mismatches 4;	Indels 2;
Gaps	2;			
Qy	1	SLALSLTADQMSALIDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV	60	
Db	5	SPVLSLTAEQMTSALLDAEPPVLYSEYDATRPNEASMMGLLTNLADRELVHMINWAKRV	64	
Qy	61	PGFVDLTLLHDQVHLLLECAWLEILMIGLVWRSMHEHPGKLLFAPNLLLDNRNQKCVEGMVEI	120	
Db	65	PGFVDLSLHDQVHLLLECAWLEILMIGLVWRSMHEHPGKLLFAPNLLLDNRNQKCVEGMVEI	124	
Qy	121	FDMLLATSSRRPMNLQG- EFVCLKSIIILNSGVYTFLSSTLKSLEEKDHIHRVLDKITD	179	
Db	125	FDMLLATSSRLRMNLQGEFVCLKSIIILNSGVYTFLSSTLKSLEEKDHIHRVLDKMTD	184	
Qy	180	TLIHLMAKAGLTQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDLLEML	239	
Db	185	TLIHLMAKAGLT-L-QQHRRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDLLEML	243	
Qy	240	DAHRL	244	
Db	244	DAHRL	248	

RESULT 12
US-08-836-620A-10
; Sequence 10, Application US/08836620A
; Patent No. 5958710

```

; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Orphan receptor
; NUMBER OF SEQUENCES: 19
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,620A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/03933
; FILING DATE:
; APPLICATION NUMBER: GB 9518272.1
; FILING DATE: 08-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9605550.4
; FILING DATE: 15-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9607532.0
; FILING DATE: 11-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9609576.5
; FILING DATE: 08-MAY-1996
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
US-08-836-620A-10

Query Match 79.6%; Score 994.5; DB 2; Length
Best Local Similarity 99.0%; Pred. No. 3.7e-99;
Matches 195; Conservative 0; Mismatches 1; Indel

QY 49 ELVHMINNAKRVPGFVDLTLDQVHLLCAWLEILMIGLVWRSMEH
Db 1 ELVHMINNAKRVPGFVDLTLDQVHLLCAWLEILMIGLVWRSMEH

QY 109 NQKCKVEGMVEIFDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGV
Db 61 NQKCKVEGMVEIFDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGV

QY 168 DHHRVLDKITDTLIHLMAKAGLTQQQHQRLAQLLLILSHIRHMS
Db 121 DHHRVLDKITDTLIHLMAKAGLTQQQHQRLAQLLLILSHIRHMS

QY 228 VVPLYDLLEMLDAHRL 244
Db 181 VVPLYDLLEMLDAHRL 197

RESULT 13
US-08-836-620A-9
; Sequence 9, Application US/08836620A
; Patent No. 5958710
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Orphan receptor
; NUMBER OF SEQUENCES: 19
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,620A
; FILING DATE:
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-836-620A-9

Query Match 78.8%; Score 984.5; DB 2; Length 243;
Best Local Similarity 97.5%; Pred. No. 4.4e-98;
Matches 192; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
QY 49 ELVHMINWAKRVPGFVDLTLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDR 108
Db 1 ELVHMINWAKRVPGFVDLTLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDR 60
QY 109 NQKCKVEGMVEIFDMLLATSSRRFRMMNLQ-EFVCLKSIILLNSGVYTFLSSTLKSLEEK 167
Db 61 NQKCKVEGMVEIFDMLLATSSRRFRMMNLQGEHFVCLKSIILLNSGVYTFLSSTLKSLEEK 120
QY 168 DHIHRVLDKITDTLIHLMAKAGLTQQQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKN 227
Db 121 DHIHRVLDKITDTLIHLMAKAGLTQQQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKN 180
QY 228 VVPLYDLEMLDAHRL 244
Db 181 VVPLYDLEMLDAHRL 197

RESULT 14
US-08-836-620A-8
Sequence 8, Application US/08836620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836.620A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Rattus rattus
US-08-836-620A-8
Query Match 78.4%; Score 979.5; DB 2; Length 243;
Best Local Similarity 97.0%; Pred. No. 1.5e-97;
Matches 191; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
QY 49 ELVHMINWAKRVPGFVDLTLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDR 108
Db 1 ELVHMINWAKRVPGFVDLTLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDR 60
QY 109 NQKCKVEGMVEIFDMLLATSSRRFRMMNLQ-EFVCLKSIILLNSGVYTFLSSTLKSLEEK 167
Db 61 NQKCKVEGMVEIFDMLLATSSRRFRMMNLQGEHFVCLKSIILLNSGVYTFLSSTLKSLEEK 120
QY 168 DHIHRVLDKITDTLIHLMAKAGLTQQQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKN 227
Db 121 DHIHRVLDKITDTLIHLMAKAGLTQQQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKN 180
QY 228 VVPLYDLEMLDAHRL 244
Db 181 VVPLYDLEMLDAHRL 197

RESULT 15
US-09-893-666A-2
Sequence 2, Application US/09893666A
Patent No. 6759568
GENERAL INFORMATION:
APPLICANT: YAMASHITA, ICHIRO
TITLE OF INVENTION: High estrogen-sensitive medaka fish
FILE REFERENCE: 210217US-620-7249-0
CURRENT APPLICATION NUMBER: US/09/893,666A
CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: JP 2000-247729
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 575
TYPE: PRT
ORGANISM: Oryzias latipes
US-09-893-666A-2

Query Match 64.4%; Score 804.5; DB 4; Length 575;
Best Local Similarity 63.9%; Pred. No. 4e-78;
Matches 154; Conservative 42; Mismatches 44; Indels 1; Gaps 1;
QY 5 SLTADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRVPGFV 64
Db 268 SIPPEQVLLLLQGAEPILCSRQKLSRPTYTEVTMTLLTSMADKELVHMIWAKKLPGL 327
QY 65 DLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCKVEGMVEIFDML 124
Db 328 QLSLHDQVLLLESSWLEVMIGLIWRSIHCPGKLIFAQDLILDRNEGDCVEGMTEIFDML 387
QY 125 LATSSRRFRMMNLQ-GEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLIH 183
Db 388 LATASRRFRVLKLPKEEFVCLKAILLNSGAFSFCGTGTMEPLHNSAAVQSMLDTITDALIH 447
QY 184 LMAKAGLTQQQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLEMLDAHR 243
Db 448 YISQGYLAQEQARRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLEMLDAHR 507
QY 244 L 244
Db 508 L 508

Search completed: November 8, 2004, 08:29:27
Job time : 15.4408 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2004, 08:04:31 ; Search time 58.7592 Seconds
(without alignments)
1489.639 Million cell updates/sec

Title: US-09-830-693B-27
Perfect score: 1250
Sequence: 1 SLALSLTADQMVSALLDAEP.....CKNVVPLYDLLLEMLDAHRL 244

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Seahbed: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	DB ID	Description
1	1239.5	99.2	414	6	Aae35275 C7LBDAS f
2	1239.5	99.2	422	4	Aab61498 Protein e
3	1239.5	99.2	438	6	Aae35276 C7LBDAS f
4	1239.5	99.2	457	4	Aab61499 Protein e
5	1239.5	99.2	480	4	Aab36684 Mammalian
6	1239.5	99.2	595	2	Aay21626 Ligand bi
7	1239.5	99.2	595	4	Aag84505 Human oes
8	1239.5	99.2	595	4	Aag84513 Human oes
9	1239.5	99.2	595	4	Aag84506 Human oes
10	1239.5	99.2	595	5	Abb76378 Human nuc
11	1239.5	99.2	595	8	Adp05661 Human nuc
12	1239.5	99.2	595	8	Ado42788 Wild type
13	1239.5	99.2	595	8	Ado42830 Human oes
14	1235.5	98.8	244	3	Aab26784 Oestrogen
15	1235.5	98.8	244	3	Aab26780 Human oes
16	1235.5	98.8	595	4	Aag84509 Human oes
17	1235.5	98.8	595	8	Ado42815 Mutant hu
18	1234.5	98.8	595	8	Ado42820 Mutant hu
19	1233.5	98.7	246	5	Abj15106 LBDG1 rel
20	1233.5	98.7	595	4	Aag84507 Human oes
21	1233.5	98.7	595	8	Ado42789 Mutant hu
22	1232.5	98.6	595	4	Aag84508 Human oes
23	1232.5	98.6	595	4	Aag84514 Human oes
24	1231.5	98.5	595	4	Aag84512 Human oes
25	1231.5	98.5	660	5	Abb76379 Cre recom

26	1230.5	98.4	347	5	ABP70164	Abp70164 Amino aci
27	1230.5	98.4	414	6	AAE35278	Aae35278 C7LBDAS f
28	1230.5	98.4	438	6	AAE35281	Aae35281 C7LBDAS f
29	1230.5	98.4	511	7	ADE39222	Ade39222 LexA-oes
30	1230.5	98.4	547	5	AAU98984	Aau98984 Oestrogen
31	1230.5	98.4	589	7	ADB99352	Adb99352 Fusion pr
32	1230.5	98.4	595	2	AAAY33506	Aay33506 Human est
33	1230.5	98.4	595	4	AAG84511	Aag84511 Human oes
34	1230.5	98.4	595	4	AAG84510	Aag84510 Human oes
35	1230.5	98.4	595	5	AAG68251	Aag68251 Human oes
36	1230.5	98.4	595	5	AAU98987	Aau98987 Oestrogen
37	1230.5	98.4	595	5	AAU98983	Aau98983 Oestrogen
38	1230.5	98.4	595	5	AAU98988	Aau98988 Oestrogen
39	1230.5	98.4	595	5	ABB09265	Abb09265 Human oes
40	1230.5	98.4	595	5	ABP70163	Abp70163 Amino aci
41	1230.5	98.4	595	5	ABB81783	Abb81783 Human oes
42	1230.5	98.4	595	6	ABG76090	Abg76090 Human oes
43	1230.5	98.4	595	6	ABR47448	AbR47448 Breast ca
44	1230.5	98.4	595	6	ABU09033	Abu09033 Human oes
45	1230.5	98.4	595	6	AAE35283	Aae35283 Human wil

ALIGNMENTS

RESULT 1
AAE35275
ID AAE35275 standard; protein; 414 AA.
XX

AC AAE35275;

XX
DT 28-MAY-2003 (first entry)

XX
DE C7LBDAS fusion (wild-type) protein.

XX
KW Oestrogen receptor; ER alpha; ligand binding domain; genetic disease;
KW acquired disease; cell proliferative disorder; cancer; adenocarcinoma;
KW LBD; gene switch; transgenic animal; transgenic; gene therapy; human;
KW zinc finger array; C7; fusion protein.

XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.

XX
PN WO200297050-A2.

XX
PD 05-DEC-2002.

XX
PF 31-MAY-2002; 2002WO-US016946.

XX
PR 31-MAY-2001; 2001US-0294839P.

XX
PA (NOVS) NOVARTIS AG.

PI Bracken KR, De Los Angeles JE, Huang Y, Kadan MJ, Ksander GM;
PI Zerby DB;

XX
DR WPI; 2003-156794/15.
DR N-PSDB; AAD53875.

XX
PT New mutant estrogen receptor ligand binding domain capable of interacting
PT with non-endogenous ligand, useful e.g. in combination with a ligand for
PT constructing selective molecular gene switches for regulating gene
PT function.

XX
PS Example 4; Page 117-118; 159pp; English.

XX
CC The invention relates to a mutant oestrogen receptor (ER) alpha-ligand
CC binding domain (LBD) which comprises an amino acid modification in region
CC 1, region 2 or both and interacting with a non-endogenous ligand as a
CC result of the amino acid modification. Sequences of the invention are
CC useful for treatment of genetic diseases, acquired diseases and any other
CC conditions including cell proliferative disorders such as cancer e.g.

CC The invention relates to a mutant oestrogen receptor (ER) alpha-ligand
CC binding domain (LBD) which comprises an amino acid modification in region
CC 1, region 2 or both and interacting with a non-endogenous ligand as a
CC result of the amino acid modification. Sequences of the invention are
CC useful for treatment of genetic diseases, acquired diseases and any other
CC conditions including cell proliferative disorders such as cancer e.g.
CC lung, breast, lymphoid, gastrointestinal, genito-urinary tract
CC adenocarcinomas and other malignancies such as colon cancers, renal- cell
CC carcinoma, prostate cancer, non-small cell carcinoma of the lung, cancer
CC of the small intestine and cancer of the oesophagus. The invention is
CC useful for constructing selective molecular gene switches for regulating
CC gene function in plants and transgenic animals. It is also useful in gene
CC therapy. The present sequence is human ER alpha LBD -zinc finger array
CC (C7) fusion protein
XX
SQ Sequence 438 AA;

Query Match 99.2%; Score 1239.5; DB 6; Length 438;
Best Local Similarity 99.6%; Pred. No. 2.3e-124;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 146 SLALSLTADQMVSAALLDAEPPILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRV 205
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCGVEGMVEI 120
Db 206 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCGVEGMVEI 265
QY 121 FDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 266 FDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 325
QY 180 TLIHLMKAGLTQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLEML 239
Db 326 TLIHLMKAGLTQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLEML 385
QY 240 DAHRL 244
Db 386 DAHRL 390

RESULT 4
AAB61499
ID AAB61499 standard; protein; 457 AA.
XX
AC AAB61499;
D 04-APR-2001 (first entry)
XX Protein encoded by human estrogen receptor alpha isoform #2.
DE Human; estrogen receptor alpha; cancer; osteoporosis; bone; Alzheimer's;
KW cardiovascular.
XX Homo sapiens.
OS WO200100823-A1.
PN 04-JAN-2001.
XX 27-JUN-2000; 2000WO-EP005981.
PF 29-JUN-1999; 99IT-MI001433.
PR (EUMO-) EURO MOLECULAR BIOLOGY LAB.
XX Gannon F, Denger S, Flouriot G;
PI WPI; 2001-137955/14.
XX Novel isoforms of human estrogen receptor alpha useful for preparing
PT therapeutic agents for treating cancer, osteoporosis, Alzheimer's disease

PT and cardiovascular diseases.
XX Claim 4; Page 46-48; 53pp; English.
PS The present invention relates to a human estrogen receptor (hER)-alpha
CC isoform. Molecules which modulate the activity of the estrogen receptor
CC are useful for the preparation of therapeutic agents for treating cancer,
CC osteoporosis and other bone disorders, Alzheimer's disease and
CC cardiovascular diseases
XX Sequence 457 AA;

Query Match 99.2%; Score 1239.5; DB 4; Length 457;
Best Local Similarity 99.6%; Pred. No. 2.4e-124;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 167 SLALSLTADQMVSAALLDAEPPILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRV 226
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCGVEGMVEI 120
Db 227 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCGVEGMVEI 286
QY 121 FDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 287 FDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 346
QY 180 TLIHLMKAGLTQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLEML 239
Db 347 TLIHLMKAGLTQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLEML 406
QY 240 DAHRL 244
Db 407 DAHRL 411

RESULT 5
AAB36684
ID AAB36684 standard; protein; 480 AA.
XX
AC AAB36684;
XX 15-MAR-2001 (first entry)
DT Mammalian two-hybrid protein SEQ ID NO:8.
DE Mammalian; two-hybrid assay; hybrid protein; hybrid gene; detection;
KW reporter gene; DNA-binding region; transcriptional activation;
KW fused protein; protein interaction.
XX Mammalia.
OS Synthetic.
XX WO200071743-A1.
PN 30-NOV-2000.
XX 25-MAY-2000; 2000WO-JP003353.
PF 25-MAY-1999; 99JP-00144946.
PR (EISA) EISAI CO LTD.
XX Tsukahara K, Hida T, Nakamura K, Yoshitomi H;
PI WPI; 2001-025169/03.
DR N-PSDB; AAC88199.
XX Novel two hybrid detection method comprising fusing two proteins with a
PT DNA binding sequence and a transcription activation sequence respectively
PT for detecting interaction of the proteins in mammalian cells.
XX

Example 2; Page 35-37; 63pp; Japanese.

The present invention describes a method for detecting the interaction of a first and a second protein within a mammalian cell. The method comprises a fusion protein of the first protein with two or more transcription activation sequences (which may be the same or different), and a fusion protein of the second protein with a DNA-binding sequence. These are expressed in a mammalian cell containing DNA carrying a reporter gene downstream of a sequence binding to the DNA-binding sequence; and the expression of the reporter gene is detected to indicate interaction of the two proteins. The method is useful for the identification and examination of protein interactions within the mammalian cell, and screening of potential drugs targeting them. The present sequence represents a hybrid protein from an example given in the present invention

Sequence 480 AA;

RESULT 6
AAV21626
ID AAY21626 standard; protein; 595 AA.
XX
XX AC AAY21626;
XX
XX -AUG-1999 (first entry)
XX
XX Ligand binding domain of nuclear receptor hER.
XX
XX Thyroid hormone receptor; aromatic compound; ligand binding domain;
KW alpha-glycerophosphate dehydrogenase; cardiac; obesity; triglyceride;
KW plasma cholesterol; anti-hypertriglyceridaemic; atherosclerosis; GPDH;
KW thyroid hormone replacement therapy; nuclear receptor.
XX
XX Homo sapiens.
OS
XX
XX WO9926966-A2.
PN
XX
XX 03-JUN-1999.
PD
XX
XX 25-NOV-1998; 98WO-US025296.
PF
XX
XX 26-NOV-1997; 97US-00980115.
PR
XX
XX (REGC) UNIV CALIFORNIA.
PA
XX
XX Scanlan TS, Baxter JD, Fletterick RJ, Wagner RL, Kushner PJ;
PI Aprelletti JW, West BL, Shiau AK;
XX

WPI; 1999-357810/30.

Modulating activity of a thyroid hormone receptor.

Disclosure; Fig 3G-R; 447pp; English.

The invention relates to a method for modulating activity of a thyroid hormone receptor that comprises administration of an aromatic compound which fits spatially and preferentially into a thyroid hormone ligand binding domain. The aromatic compound (of a specified formula) can be used to increase alpha-glycerophosphate dehydrogenase (GPDH) levels, at levels which do not significantly modify cardiac GPDH levels and are indicated in the treatment of obesity. The compound also lower total plasma cholesterol and triglyceride levels and can be used as anti-hypertriglyceridaemic agents. The compound may also be used for treating atherosclerosis and may be indicated in thyroid hormone replacement therapy in patients with compromised cardiac function. Sequences AAY21621 - 636 amino acid sequences of ligand binding domains of several members of the nuclear receptor superfamily

Sequence 595 AA;

RESULT 7	
AAG84505	
ID	AAG84505 standard; protein; 595 AA.
XX	
XX	AAG84505;
XX	
DT	10-SEP-2001 (first entry)
XX	
DE	Human oestrogen receptor alpha protein.
XX	
KW	Ligand dependent transcriptional factor; oestrogen receptor; ER;
KW	glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;
KW	MR; peroxisome proliferator-activated receptor protein; PPAR;
KW	progesterone receptor protein; PR; pregnane X receptor protein; PXR;
KW	thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;
KW	transactivation; ERalpha; breast cancer.
XX	
OS	Homo sapiens.
XX	
PN	WO200142307-A1.
XX	
PD	14-JUN-2001.
XX	
PF	01-DEC-2000; 2000WO-JP008553.
XX	
PR	07-DEC-1999; 99JP-00348022.

PR 27-DEC-1999; 99JP-00370667.
PR 07-JUL-2000; 2000JP-00207011.
PR 21-JUL-2000; 2000JP-00220508.
PR 02-AUG-2000; 2000JP-00234053.
PR 03-AUG-2000; 2000JP-00235460.
PR 03-AUG-2000; 2000JP-00235461.
PR 03-AUG-2000; 2000JP-00235463.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
XX Saito K, Ohe N, Satoh H;
XX WPI; 2001-367866/38.
DR
XX
XX
PT Ligand dependent transcriptional factors, nucleic acids encoding them and
PT cells comprising them and a specified reporter gene, useful for screening
PT agents for the treatment of breast cancer.
XX
PS Claim 7; Page 167-170; 276pp; English.
XX
CC The present invention relates to ligand dependent transcriptional factors
CC including oestrogen receptor (ER) alpha and beta protein, glucocorticoid
CC receptor protein (GR), mineralocorticoid receptor protein (MR),
CC peroxisome proliferator-activated receptor protein (PPAR), progesterone
CC receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone
CC receptor protein (TR) and vitamin D receptor protein (VDR), the nucleic
CC acids encoding them and cells comprising them and a specified reporter
CC gene for the ligand dependent transcriptional factor. These proteins are
CC useful in the modulation of ligand dependent transcriptional factor
CC activity. The cells, mutant ERalpha and the polynucleotide encoding it
CC may be used in assays for qualitatively analysing an activity for
CC transactivation of a reporter gene by a test ERalpha, for screening
CC mutant ligand dependent transcriptional factors, for evaluating an
CC activity for transactivation of a reporter gene by a test ERalpha and/or
CC for screening a compound useful for treating a disorder of a mutant
CC ERalpha, especially breast cancer
XX
SQ Sequence 595 AA;

Query Match 99.2%; Score 1239.5; DB 4; Length 595;
Best Local Similarity 99.6%; Pred. No. 3.5e-124;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSSEASMMGLLTNLADRELVHMINWAKRV 60
DB |||||
DB 305 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSSEASMMGLLTNLADRELVHMINWAKRV 364
DB |||||
DB 61 PGFVDLTLDHQQVHLLCAWLEILMIGLVWRSMHPGKLLFAPNLLDRNQKCVGMEI 120
DB |||||
DB 365 PGFVDLTLDHQQVHLLCAWLEILMIGLVWRSMHPGKLLFAPNLLDRNQKCVGMEI 424
QY 121 FDMLLATSSRRFRMNLQGG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
DB |||||
DB 425 FDMLLATSSRRFRMNLQGG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484
QY 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRMSNKGMEHLYSMCKKNVVPVLYDLLLLLEML 239
DB |||||
DB 485 TLIHLMKAGLTQQQHQRQAQLLLILSHIRMSNKGMEHLYSMCKKNVVPVLYDLLLLLEML 544
QY 240 DAHRL 244
DB |||||
DB 545 DAHRL 549

RESULT 8
AAG84513
ID AAG84513 standard; protein; 595 AA.
XX
AC AAG84513;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human oestrogen receptor alpha protein mutant S578P.

XX
KW Ligand dependent transcriptional factor; oestrogen receptor; ER;
KW glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;
KW MR; peroxisome proliferator-activated receptor protein; PPAR;
KW progesterone receptor protein; PR; pregnane X receptor protein; PXR;
KW thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;
KW transactivation; ERalpha; breast cancer; mutant; mutein.
XX
OS Homo sapiens.
XX
XX WO2001142307-A1.
XX
XX 14-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-JP008553.
XX
XX 07-DEC-1999; 99JP-00348022.
XX 27-DEC-1999; 99JP-00370667.
XX 07-JUL-2000; 2000JP-00207011.
XX 21-JUL-2000; 2000JP-00220508.
XX 02-AUG-2000; 2000JP-00234053.
XX 03-AUG-2000; 2000JP-00235460.
XX 03-AUG-2000; 2000JP-00235461.
XX 03-AUG-2000; 2000JP-00235463.
XX (SUMO) SUMITOMO CHEM CO LTD.
XX
XX Saito K, Ohe N, Satoh H;
XX WPI; 2001-367866/38.
XX
XX Ligand dependent transcriptional factors, nucleic acids encoding them and
XX cells comprising them and a specified reporter gene, useful for screening
XX agents for the treatment of breast cancer.
XX
XX Claim 20; Page 194-197; 276pp; English.
XX
CC The present invention relates to ligand dependent transcriptional factors
CC including oestrogen receptor (ER) alpha and beta protein, glucocorticoid
CC receptor protein (GR), mineralocorticoid receptor protein (MR),
CC peroxisome proliferator-activated receptor protein (PPAR), progesterone
CC receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone
CC receptor protein (TR) and vitamin D receptor protein (VDR), the nucleic
CC acids encoding them and cells comprising them and a specified reporter
CC gene for the ligand dependent transcriptional factor. These proteins are
CC useful in the modulation of ligand dependent transcriptional factor
CC activity. The cells, mutant ERalpha and the polynucleotide encoding it
CC may be used in assays for qualitatively analysing an activity for
CC transactivation of a reporter gene by a test ERalpha, for screening
CC mutant ligand dependent transcriptional factors, for evaluating an
CC activity for transactivation of a reporter gene by a test ERalpha and/or
CC for screening a compound useful for treating a disorder of a mutant
CC ERalpha, especially breast cancer
XX
SQ Sequence 595 AA;

Query Match 99.2%; Score 1239.5; DB 4; Length 595;
Best Local Similarity 99.6%; Pred. No. 3.5e-124;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSSEASMMGLLTNLADRELVHMINWAKRV 60
DB |||||
DB 305 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDHQQVHLLCAWLEILMIGLVWRSMHPGKLLFAPNLLDRNQKCVGMEI 120
DB |||||
DB 365 PGFVDLTLDHQQVHLLCAWLEILMIGLVWRSMHPGKLLFAPNLLDRNQKCVGMEI 424
QY 121 FDMLLATSSRRFRMNLQGG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
DB |||||
DB 425 FDMLLATSSRRFRMNLQGG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484
QY 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRMSNKGMEHLYSMCKKNVVPVLYDLLLLLEML 239

Db 485 TLIHMAKAGLTQQQHQRLAQLLLSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 544

QY 240 DAHRL 244

Db 545 DAHRL 549

RESULT 9

AAG84506

ID AAG84506 standard; protein; 595 AA.

XX

AC AAG84506;

XX

DT 10-SEP-2001 (first entry)

XX

DE Human oestrogen receptor alpha protein mutant K303R.

XX

KW Ligand dependent transcriptional factor; oestrogen receptor; ER;

KW glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;

KW MR; peroxisome proliferator-activated receptor protein; PPAR;

KW progesterone receptor protein; PR; pregnane X receptor protein; PXR;

KW thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;

KW transactivation; ERalpha; breast cancer; mutant; mutein.

XX

OS Homo sapiens.

XX

XX

PN WO200142307-A1.

XX

PD 14-JUN-2001.

XX

PF 01-DEC-2000; 2000WO-JP008553.

XX

PR 07-DEC-1999; 99JP-00348022.

PR 27-DEC-1999; 99JP-00370667.

PR 07-JUL-2000; 2000JP-00207011.

PR 21-JUL-2000; 2000JP-00220508.

PR 02-AUG-2000; 2000JP-00234053.

PR 03-AUG-2000; 2000JP-00235460.

PR 03-AUG-2000; 2000JP-00235461.

PR 03-AUG-2000; 2000JP-00235463.

XX

PA (SUMO) SUMITOMO CHEM CO LTD.

XX

PI Saito K, Ohe N, Satoh H;

XX

DR WPI; 2001-367866/38.

XX

PT ligand dependent transcriptional factors, nucleic acids encoding them and

PT cells comprising them and a specified reporter gene, useful for screening

PT agents for the treatment of breast cancer.

XX

PS Claim 15; Page 170-174; 276pp; English.

XX

CC The present invention relates to ligand dependent transcriptional factors

CC including oestrogen receptor (ER) alpha and beta protein, glucocorticoid

CC receptor protein (GR), mineralocorticoid receptor protein (MR),

CC peroxisome proliferator-activated receptor protein (PPAR), progesterone

CC receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone

CC receptor protein (TR) and vitamin D receptor protein (VDR), the nucleic

CC acids encoding them and cells comprising them and a specified reporter

CC gene for the ligand dependent transcriptional factor. These proteins are

CC useful in the modulation of ligand dependent transcriptional factor

CC activity. The cells, mutant ERalpha and the polynucleotide encoding it

CC may be used in assays for qualitatively analysing an activity for

CC transactivation of a reporter gene by a test ERalpha, for screening

CC mutant ligand dependent transcriptional factors, for evaluating an

CC activity for transactivation of a reporter gene by a test ERalpha and/or

CC for screening a compound useful for treating a disorder of a mutant

CC ERalpha, especially breast cancer

XX

SQ Sequence 595 AA;

Query Match 99.2%; Score 1239.5; DB 4; Length 595;

Best Local Similarity 99.6%; Pred. No. 3.5e-124;

Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 60

Db 305 SLALSLTADQMVSAALDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 364

QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEI 120

Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEI 424

QY 121 FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179

Db 425 FDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484

QY 180 TLIHLMAGAGLTQQQHQRLAQLLLSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 239

Db 485 TLIHLMAGAGLTQQQHQRLAQLLLSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 544

QY 240 DAHRL 244

Db 545 DAHRL 549

RESULT 10

ABB76378

ID ABB76378 standard; protein; 595 AA.

XX

AC ABB76378;

XX

DT 22-AUG-2002 (first entry)

XX

DE Human nuclear oestrogen receptor alpha.

XX

KW Oestrogen; receptor; human; transgenic mouse; cytostatic;

KW antiinflammatory; antidiabetic; endocrine; anorectic; hepatotropic.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 180..262

FT /note= "DNA-binding domain"

FT Region 263..301

FT /note= "D hinge region"

FT Domain 302..552

FT /note= "ligand-binding domain"

XX

PN WO200228175-A2.

XX

PD 11-APR-2002.

XX

PF 28-SEP-2001; 2001WO-IB002246.

XX

PR 03-OCT-2000; 2000FR-00012570.

PR 11-MAY-2001; 2001US-00853033.

XX

PA (ADER-) ADEREGEM ASSOC DEV RECH EN GENETIQ.

XX

PI Chambon P, Metzger D;

XX

DR WPI; 2002-463217/49.

DR N-PSDB; ABL57497.

XX

PT A transgenic mouse, useful in screening for medicaments for the treatment

PT of e.g., diabetes or skin cancers, comprises a fusion protein between a

PT recombinase Cre, and a modified ligand binding domain of the nuclear

PT estrogen receptor alpha.

XX

PS Claim 6; Page 131-132; 149pp; English.

XX

CC The present sequence is the protein sequence of the human nuclear

CC oestrogen receptor alpha (I). The invention relates to a non-human

CC metazoan organism, especially a transgenic mouse, characterised in that
CC at least one cell comprises: (i) a fusion protein formed from a
CC recombinase (Cre), a hinge region (preferably human (I) D hinge), and a
CC modified ligand binding domain (LBD) of a nuclear oestrogen receptor,
CC especially human (I), its fragment or variant; and (ii) one or more genes
CC or DNA sequences of interest belonging to the genome of the organism,
CC into which one or more recognition sites of the recombinase protein are
CC inserted. The (I) LBD domain is preferably modified by a G521R, G400V, or
CC M543A/I544A mutation. The fusion protein has negligible, or even zero,
CC recombinase activity in the presence of a natural ligand such as
CC oestradiol, but recombinase activity is induced by a small quantity of a
CC synthetic ligand that has antioestrogenic activity, e.g. tamoxifen or 4-
CC hydroxytamoxifen. The metazoan organism or its cells, such as epidermal
CC cells, hepatocytes or adipocytes, are useful in carrying out a
CC spatiotemporally controlled site-specific recombination of a DNA sequence
CC of interest in its natural chromatin environment. It is also used in
CC screening of medicaments for pathological conditions associated with an
CC alteration of the expression and/or function of the DNA sequence of
CC interest, such as skin cancer, inflammation, diabetes, alopecia, obesity,
CC or in promoting hepatic regeneration

XX Sequence 595 AA;

Query Match 99.2%; Score 1239.5; DB 5; Length 595;
Best Local Similarity 99.6%; Pred. No. 3.5e-124;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db |||||
305 SLALSLTADQMVSAALLDAEPPILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCGVEGMVEI 120
Db |||||
365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCGVEGMVEI 424
QY 121 FDMLLATSSRRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db |||||
425 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484
QY 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLLEML 239
Db |||||
485 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLLEML 544

QY 240 DAHRL 244

Db |||||

545 DAHRL 549

RESULT 11

ADP05661

ID ADP05661 standard; protein; 595 AA.

XX AC ADP05661;

XX 26-AUG-2004 (first entry)

DT Human nuclear receptor protein SeqID35.

XX disease risk; disorder risk; mutation; polymorphism;
KW nuclear receptor protein; antibacterial; antithyroid; cardiovascular-Gen;
KW cytostatic; dermatological; eating-Disorders-Gen; gastrointestinal-Gen;
KW gynaecological; hepatotropic; immunosuppressive; muscular-Gen;
KW nephrotropic; osteopathic; virucide; adrenal gland; colon;
KW cardiovascular; intestine; kidney; liver; lung; muscular; ovary; blood;
KW prostate; skin; spleen; stomach; testes; thymus; thyroid; uterus;
KW pancreas; bone; joint; breast; immune system; metabolic;
KW nutritive disease; human.

XX Homo sapiens.

OS WO2004045369-A2.

PN 03-JUN-2004.

PD

XX 12-NOV-2003; 2003WO-US036229.
XX 14-NOV-2002; 2002US-0426305P.
XX (NURA-) NURA INC.

XX Gaitanaris GA, Bergmann JE, Gracarov A, Hohmann J, Li F;
PI Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX WPI; 2004-449627/42.
DR N-PSDB; ADP05662.

PT Determining an increased risk for e.g. colon, brain or breast disease or
PT disorder, by detecting a mutation or polymorphism in the nuclear receptor
PT gene, or measuring expression or biological activity level of the nuclear
PT receptor.

PS Claim 1; SEQ ID NO 35; 508pp; English.

XX This invention relates to a novel method of determining whether a patient
CC has an increased risk for developing a disease or disorder which
CC comprises determining the presence of a mutation or polymorphism in the
CC patient's gene encoding a nuclear receptor protein or measuring the
CC expression or level of biological activity of a nuclear receptor
CC polypeptide in the patient or in a cell of the patient. The invention may
CC be useful for the development of compounds with an antibacterial,
CC antithyroid, cardiovascular-Gen, cytostatic, dermatological, eating-
CC Disorders-Gen, gastrointestinal-Gen, gynaecological, hepatotropic,
CC immunosuppressive, muscular-Gen, nephrotropic, osteopathic or virucide
CC activity. The method is useful for determining whether a patient has an
CC increased risk for developing a disease or disorder. The nucleic acid
CC encoding a nuclear receptor polypeptide, an expression vector comprising
CC the nucleic acid operably linked to a promoter, or a compound that
CC modulates the biological activity of a nuclear receptor polypeptide, is
CC useful for treating or preventing a disease or disorder of the adrenal
CC gland, colon, cardiovascular, intestine, kidney, liver, lung, muscular,
CC ovary, blood, prostate, skin, spleen, stomach, testes, thymus, thyroid,
CC uterus, pancreas, bone and joints, breast, or immune system, or metabolic
CC or nutritive disease or disorder. The present sequence is that of a
CC nuclear receptor protein which may be used in the method of the
CC invention.

XX Sequence 595 AA;

Query Match 99.2%; Score 1239.5; DB 8; Length 595;
Best Local Similarity 99.6%; Pred. No. 3.5e-124;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db |||||
305 SLALSLTADQMVSAALLDAEPPILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCGVEGMVEI 120
Db |||||
365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCGVEGMVEI 424
QY 121 FDMLLATSSRRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db |||||
425 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484
QY 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLLEML 239
Db |||||
485 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLLEML 544
QY 240 DAHRL 244
Db |||||

545 DAHRL 549

RESULT 12

ADO42788

ID ADO42788 standard; protein; 595 AA.

XX ADO42788;
AC 26-AUG-2004 (first entry)
XX
DT
XX
DE
XX
XX Wild type human oestrogen receptor-alpha (ER) protein.
DE
XX human; oestrogen receptor-alpha; ER; ER activity regulator substance;
KW anti-oestrogen substance.
KW
XX
OS Homo sapiens.
OS
XX WO2004046352-A1.
XX
PN 03-JUN-2004.
PD
XX
XX 14-NOV-2003; 2003WO-JP014494.
PF
XX 15-NOV-2002; 2002JP-00331994.
PR
XX 15-NOV-2002; 2002JP-00331994.
PR
XX 15-NOV-2002; 2002JP-00331995.
PR
XX 15-NOV-2002; 2002JP-00331996.
PR
XX (SUMO) SUMITOMO CHEM CO LTD.
PA
XX Fujimori K;
PI
XX WPI; 2004-431978/40.
DR
XX New mutant estrogen receptor-alpha useful for determining effectiveness
PT of treatment by estrogen receptor activity regulator substance and
PT antiestrogen substance.
PT
XX Claim 1; SEQ ID NO 1; 111pp; Japanese.
PS
XX The invention comprises the amino acid sequences of mutant human
XX oestrogen receptor-alpha (ER) proteins. The mutant ER proteins of the
CC invention are useful for determining the effectiveness of a treatment by
CC an ER activity regulator substance, and for determining the effectiveness
CC of a treatment by an anti-oestrogen substance. The present amino acid
CC sequence represents the wild-type human ER protein.
XX
SQ Sequence 595 AA;
Query Match 99.2%; Score 1239.5; DB 8; Length 595;
Best Local Similarity 99.6%; Pred. No. 3.5e-124;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 SLALSITADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSITADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 364
Qy 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVGMEVEI 120
Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVGMEVEI 424
Qy 121 FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 425 FDMLLATSSRFRMMNLQGEFEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484
Qy 180 TLIHLMKAGLTLQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 239
Db 485 TLIHLMKAGLTLQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 544
Qy 240 DAHRL 244
Db 545 DAHRL 549
RESULT 13
ADO42830
ID ADO42830 standard; protein; 595 AA.
XX
AC ADO42830;
DT 18-JAN-2001 (first entry)

XX 26-AUG-2004 (first entry)
DT
XX Human oestrogen receptor-alpha (ER) protein.
DE
XX
KW human; oestrogen receptor-alpha; ER; ER activity regulator substance;
KW anti-oestrogen substance.
XX
OS Homo sapiens.
OS
XX WO2004046352-A1.
PN
XX 03-JUN-2004.
PD
XX
XX 14-NOV-2003; 2003WO-JP014494.
PF
XX 15-NOV-2002; 2002JP-00331994.
PR
XX 15-NOV-2002; 2002JP-00331995.
PR
XX 15-NOV-2002; 2002JP-00331996.
PR
XX (SUMO) SUMITOMO CHEM CO LTD.
PA
XX Fujimori K;
PI
XX WPI; 2004-431978/40.
DR
XX New mutant estrogen receptor-alpha useful for determining effectiveness
PT of treatment by estrogen receptor activity regulator substance and
PT antiestrogen substance.
PT
XX Disclosure; Fig 19; 111pp; Japanese.
PS
XX The invention comprises the amino acid sequences of mutant human
XX oestrogen receptor-alpha (ER) proteins. The mutant ER proteins of the
CC invention are useful for determining the effectiveness of a treatment by
CC an ER activity regulator substance, and for determining the effectiveness
CC of a treatment by an anti-oestrogen substance. The present amino acid
CC sequence represents a human ER protein.
XX
SQ Sequence 595 AA;
Query Match 99.2%; Score 1239.5; DB 8; Length 595;
Best Local Similarity 99.6%; Pred. No. 3.5e-124;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 SLALSITADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSITADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 364
Qy 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVGMEVEI 120
Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVGMEVEI 424
Qy 121 FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
Db 425 FDMLLATSSRFRMMNLQGEFEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484
Qy 180 TLIHLMKAGLTLQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 239
Db 485 TLIHLMKAGLTLQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 544
Qy 240 DAHRL 244
Db 545 DAHRL 549
RESULT 14
AAB26784
ID AAB26784 standard; protein; 244 AA.
XX
AC AAB26784;
XX
DT 18-JAN-2001 (first entry)

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XX DE Oestrogen receptor protein sequence.
XX KW Homology model; ligand binding domain; glucocorticoid receptor; AIDS;
XX KW hypertension; diabetes; obesity; glaucoma; depression; wound;
XX KW protein co-ordinate data; thyroid hormone receptor; oestrogen receptor.
XX OS Unidentified.
XX PN WO200052050-A2.
XX PD 08-SEP-2000.
XX PF 01-MAR-2000; 2000WO-GB0000727.
XX PR 01-MAR-1999; 99GB-00004441.
XX PR 22-APR-1999; 99GB-00009151.
XX PA (KARO-) KARO BIO AB.
XX PI Gillner M, Greenidge P;
XX XX WPI; 2000-549565/50.
XX DR Designing a homology model of the ligand binding domain of a
XX PT glucocorticoid receptor displayed as a three-dimensional image, useful
XX PT for identifying agonists and antagonists for treating e.g. inflammation,
XX PT hypertension, glaucoma, diabetes.
XX PS Disclosure; Fig 6; 246pp; English.
XX XX
XX CC This invention relates to a method for designing an homology model of the
XX CC ligand binding domain of a glucocorticoid receptor. The homology model
XX CC may be displayed as a three-dimensional image. The method comprises: (a)
XX CC providing an amino acid sequence and an x-ray crystallographic structure
XX CC of the ligand binding domain of a thyroid, oestrogen or progesterone
XX CC receptor; (b) modifying the x-ray crystallographic structure to take
XX CC account of differences between the amino acid configuration of the ligand
XX CC binding domain of the glucocorticoid receptor and the thyroid, oestrogen,
XX CC or progesterone receptor; (c) verifying the accuracy of the homology
XX CC model by comparing it with experimentally-determined binding properties
XX CC of a number of ligands for the glucocorticoid receptor; and (d) modifying
XX CC the homology model for greater consistency with the binding properties.
XX CC The homology model is useful for drug screening and designing ligands
XX CC (agonists and antagonists) capable of binding to a glucocorticoid
XX CC receptor. The identified agonists are useful for the treatment of
XX CC inflammation and also in immunosuppressive therapy. The identified
XX CC antagonists are useful for the treatment of hypertension, diabetes,
XX CC obesity, glaucoma, depression, acquired immune deficiency syndrome (AIDS)
XX CC and wounds. The homology models are also useful for electronic screening
XX CC of compound databases, de novo drug design and/or prediction of binding
XX CC affinities of glucocorticoid receptor ligands for the receptor by
XX CC molecular mechanics scoring functions. The specification contains protein
XX CC co-ordinate data for the glucocorticoid receptor models produced using
XX CC the method, based on the x-ray crystallographic structure of the
XX CC oestrogen and progesterone receptors. The present sequence represents an
XX CC oestrogen receptor protein. The protein is used in an example of the
XX CC method of the invention for homology modelling of a glucocorticoid
XX CC receptor based on the thyroid and oestrogen receptors
XX SQ
XX Sequence 244 AA;
XX Query Match 98.8%; Score 1235.5; DB 3; Length 244;
XX Best Local Similarity 99.6%; Pred. No. 2.8e-124;
XX Matches 243; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX QY 1 SLALSLTADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
XX DB |||||
XX QY 1 SLALSLTADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
XX DB |||||
XX QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMVEI 120
XX DB |||||
XX QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMVEI 120
XX DB |||||
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QY 121 FDMLLATSSRRFRMMNLQG-EFVCLKSIILLNSGVYFSLSTLKSLEEKDHIHRVLDKITD 179
Db |||||
QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYFSLSTLKSLEEKDHIHRVLDKITD 180
Db |||||
QY 180 TLIHLMAGAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKNVVPLYDLLEML 239
Db |||||
QY 181 TLIHLMAGAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKNVVPLYDLLEML 240
QY 240 DAHR 243
Db |||||
Db 241 DAHR 244
XX RESULT 15
XX AAB26780
XX ID AAB26780 standard; protein; 244 AA.
XX AC AAB26780;
XX XX
XX DT 18-JAN-2001 (first entry)
XX DE Human oestrogen receptor protein sequence.
XX KW Homology model; ligand binding domain; glucocorticoid receptor; AIDS;
XX KW hypertension; diabetes; obesity; glaucoma; depression; wound; human;
XX KW protein co-ordinate data; thyroid hormone receptor; oestrogen receptor.
XX OS Homo sapiens.
XX PN WO200052050-A2.
XX PD 08-SEP-2000.
XX PF 01-MAR-2000; 2000WO-GB0000727.
XX PR 01-MAR-1999; 99GB-00004441.
XX PR 22-APR-1999; 99GB-00009151.
XX PA (KARO-) KARO BIO AB.
XX PI Gillner M, Greenidge P;
XX XX WPI; 2000-549565/50.
XX PT Designing a homology model of the ligand binding domain of a
XX PT glucocorticoid receptor displayed as a three-dimensional image, useful
XX PT for identifying agonists and antagonists for treating e.g. inflammation,
XX PT hypertension, glaucoma, diabetes.
XX PS Disclosure; Fig 2A; 246pp; English.
XX XX
XX CC This invention relates to a method for designing an homology model of the
XX CC ligand binding domain of a glucocorticoid receptor. The homology model
XX CC may be displayed as a three-dimensional image. The method comprises: (a)
XX CC providing an amino acid sequence and an x-ray crystallographic structure
XX CC of the ligand binding domain of a thyroid, oestrogen or progesterone
XX CC receptor; (b) modifying the x-ray crystallographic structure to take
XX CC account of differences between the amino acid configuration of the ligand
XX CC binding domain of the glucocorticoid receptor and the thyroid, oestrogen,
XX CC or progesterone receptor; (c) verifying the accuracy of the homology
XX CC model by comparing it with experimentally-determined binding properties
XX CC of a number of ligands for the glucocorticoid receptor; and (d) modifying
XX CC the homology model for greater consistency with the binding properties.
XX CC The homology model is useful for drug screening and designing ligands
XX CC (agonists and antagonists) capable of binding to a glucocorticoid
XX CC receptor. The identified agonists are useful for the treatment of
XX CC inflammation and also in immunosuppressive therapy. The identified
XX CC antagonists are useful for the treatment of hypertension, diabetes,
XX CC obesity, glaucoma, depression, acquired immune deficiency syndrome (AIDS)
XX CC and wounds. The homology models are also useful for electronic screening
XX CC of compound databases, de novo drug design and/or prediction of binding
XX CC affinities of glucocorticoid receptor ligands for the receptor by
```


CC molecular mechanics scoring functions. The specification contains protein
CC co-ordinate data for the glucocorticoid receptor models produced using
CC the method, based on the X-ray crystallographic structure of the
CC oestrogen and progesterone receptors. The present sequence represents the
CC human oestrogen receptor protein. The protein is used in an example of
CC the method of the invention for homology modelling based on the thyroid
CC receptor

XX

SQ Sequence 244 AA;

Query Match 98.8%; Score 1235.5; DB 3; Length 244;
Best Local Similarity 99.6%; Pred. No. 2.8e-124;
Matches 243; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	1	SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV	60
Db	1	SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV	60
Qy	61	PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGVEI	120
Db	61	PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGVEI	120
Qy	121	FDMLLATSSRRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD	179
Db	121	FDMLLATSSRRFRMMNLQGEFEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD	180
Qy	180	TLIHLMAKAGLTLOQOQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEML	239
Db	181	TLIHLMAKAGLTLOQOQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEML	240
Qy	240	DAHR 243	
Db	241	DAHR 244	

Search completed: November 8, 2004, 08:26:23
Job time : 60.7592 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 8, 2004, 08:05:27 ; Search time 45.1837 Seconds
(without alignments)
3132.595 Million cell updates/sec

Title: US-09-830-693B-28
Perfect score: 1230
Sequence: 1 SLALSLTADQMVSALLDAEP.....CKNVVPLYDLLLEMLDAHRL 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1206.5	98.1	595	1 ESR1_HUMAN	P03372 homo sapien
2	1175.5	95.6	596	2 Q6QIS5	Q6qis5 bos taurus
3	1175.5	95.6	596	2 AAS46251	Aas46251 bos taurus
4	1171.5	95.2	599	1 ESR1_MOUSE	P19785 mus musculus
5	1167.5	94.9	600	1 ESR1_RAT	P06211 rattus norv
6	1164.5	94.7	595	1 ESR1_PIG	Q29040 sus scrofa
7	1159.5	94.3	595	1 ESR1_MESAU	Q9qzj5 mesocricetu
8	1146.5	93.2	587	2 Q8UWB0	Q8uwb0 caiman croc
9	1146	93.2	594	1 ESR1_HORSE	Q9tv98 equus cabal
10	1144.5	93.0	587	1 ESR1_POEGU	P01250 poephila gu
11	1143.5	93.0	589	1 ESR1_CHICK	P06212 gallus gall
12	1142.5	92.9	587	2 Q765N7	Q765n7 alligator m
13	1142.5	92.9	587	2 BAD08348	Bad08348 alligator
14	1139.5	92.6	589	2 Q8AYH0	Q8ayh0 coturnix co
15	1137.5	92.5	353	2 Q8CGK8	Q8cgk8 cavia porce
16	1137.5	92.5	431	2 Q95L13	Q95l13 ovis aries
17	1110.5	90.3	581	2 Q8UWA9	Q8uwa9 cnemidophor
18	1103.5	89.7	349	1 ESR1_ANOCA	Q9yht3 anolis caro
19	1042.5	84.8	427	2 Q6W5G5	Q6w5g5 xenopus lae
20	1042.5	84.8	427	2 AAQ84784	Aaq84784 xenopus l
21	1042.5	84.8	543	2 Q6W5G9	Q6w5g9 xenopus tro
22	1042.5	84.8	543	2 AAQ84780	Aaq84780 xenopus t
23	1042.5	84.8	585	2 Q6W5G7	Q6w5g7 xenopus lae
24	1042.5	84.8	585	2 AAQ84782	Aaq84782 xenopus l
25	1037.5	84.3	586	1 ESR1_XENLA	P81559 xenopus lae
26	1033.5	84.0	427	2 Q6W5G6	Q6w5g6 xenopus lae
27	1033.5	84.0	427	2 AAQ84783	Aaq84783 xenopus l
28	992.5	80.7	307	1 ESR1_CNEUN	Q91424 cnemidophor
29	830	67.5	542	2 Q90ZE6	Q90ze6 squalus aca
30	828.5	67.4	174	1 ESR1_BOVIN	P49884 bos taurus
31	811.5	66.0	570	2 Q800Q2	Q800q2 zoarces viv

RESULT 1
ESR1_HUMAN
ID ESR1_HUMAN STANDARD; PRT; 595 AA.
AC P03372; Q13511; Q14276; Q9NU51; Q9UDZ7; Q9UIS7;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
GN Name=ESR1; Synonyms=NR3A1, ESR;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX MEDLINE=86122927; PubMed=3753802;
RA Greene G.L., Gilna P., Waterfield M., Baker A., Hort Y., Shine J.;
RT "Sequence and expression of human estrogen receptor complementary
RT DNA.";
RL Science 231:1150-1154(1986).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX MEDLINE=86146892; PubMed=3754034;
RA Green S., Walter P., Kumar V., Krust A., Bornert J.-M., Argos P.,
RA Chambon P.;
RT "Human oestrogen receptor cDNA: sequence, expression and homology to
RT v-erb-A.";
RL Nature 320:134-139(1986).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANT ASP-411 INS.
RC TISSUE=Breast;
RX MEDLINE=96174665; PubMed=8600466;
RA Pink J.J., Wu S.Q., Wolf D.M., Billimoria M.M., Jordan V.C.;
RT "A novel 80 kDa human estrogen receptor containing a duplication of
RT exons 6 and 7.";
RL Nucleic Acids Res. 24:962-969(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANT SER-77.
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.;
RT "NIHS-SNPs, environmental genome project, NIHS ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 152-595 FROM N.A. (ISOFORM LONG).
RX MEDLINE=20084372; PubMed=10619354;
RA Schubert E.L., Lee M.K., Newman B., King M.C.;
RT "Single nucleotide polymorphisms (SNPs) in the estrogen receptor gene
RT and breast cancer susceptibility.";
RL J. Steroid Biochem. Mol. Biol. 71:21-27(1999).
RN [6]
RP SEQUENCE OF 216-434 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Breast carcinoma;

ALIGNMENTS

32	808.5	65.7	627	2	Q9DDZ4	Q9ddz4 micropterus
33	808.5	65.7	627	2	AAG44622	Aag44622 micropter
34	806.5	65.6	574	2	Q7T2K8	Q7t2k8 halichoeres
35	799.5	65.0	620	2	Q7SZI0	Q7szio fundulus he
36	797.5	64.8	581	1	ESR1_PAGMA	O42132 pagrus majo
37	796.5	64.8	525	1	ESR1_MICUN	P57753 micropogoni
38	794.5	64.6	579	1	ESR1_SPAAU	Q9pvz9 sparus aura
39	792.5	64.4	620	1	ESR1_ORYLA	P50241 oryzias lat
40	789.5	64.2	583	2	Q804Q6	Q804q6 acanthopagr
41	789	64.1	310	2	Q6MZQ9	Q6mzg9 homo sapien
42	789	64.1	310	2	CAE45969	Cae45969 homo sapi
43	786	63.9	578	2	Q8QHL0	Q8qhl0 paralichthy
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45	784.5	63.8	585	1	ESR1_ORENI	Q9yh33 oreochromis

RX MEDLINE=93153765; PubMed=7916651;
RA Pfeffer U., Pecarotta E., Castagnetta L., Vidali G.;
RT "Estrogen receptor variant messenger RNA lacking exon 4 in estrogen-
RT responsive human breast cancer cell lines.";
RL Cancer Res. 53:741-743(1993).
RN [7]
RP SEQUENCE OF 110-117, PHOSPHORYLATION, AND MUTAGENESIS.
RX MEDLINE=96026869; PubMed=7476978;
RA Joel P.B., Traish A.M., Lannigan D.A.;
RT "Estradiol and phorbol ester cause phosphorylation of serine 118 in
RT the human estrogen receptor.";
RL Mol. Endocrinol. 9:1041-1052(1995).
RN [8]
RP SEQUENCE OF 354-548 FROM N.A.
RC TISSUE=Breast carcinoma;
RA Naundorf H., Becker M., Fiebig C., Buettner B., Fichtner I.;
RT "Mechanisms of acquired tamoxifen resistance in a xenotransplanted
RT human breast carcinoma.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE OF 413-595 FROM N.A.
RA Parker A.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE OF 532-542, AND PHOSPHORYLATION.
RX MEDLINE=95280953; PubMed=7539106;
RA Arnold S.F., Obourn J.D., Jaffe H., Notides A.C.;
RT "Phosphorylation of the human estrogen receptor on tyrosine 537 in
RT vivo and by src family tyrosine kinases in vitro.";
RL Mol. Endocrinol. 9:24-33(1995).
RN [11]
RP INTERACTION WITH NCOA6.
RX MEDLINE=20036574; PubMed=10567404;
RA Lee S.-K., Anzick S.L., Choi J.-E., Bubendorf L., Guan X.-Y.,
RA Jung Y.-K., Kallioniemi O.P., Kononen J., Trent J.M., Azorsa D.,
RA Chun B.-H., Cheong J.H., Lee Y.C., Meltzer P.S., Lee J.W.;
RT "A nuclear factor ASC-2, as a cancer-amplified transcriptional
RT coactivator essential for ligand-dependent transactivation by nuclear
RT receptors in vivo.";
RL J. Biol. Chem. 274:34283-34293(1999).
RN [12]
RP INTERACTION WITH NCOA5.
RX MEDLINE=20565767; PubMed=11113208; DOI=10.1128/MCB.21.1.343-353.2001;
RA Sauve F., McBroom L.D.B., Gallant J., Moraitis A.N., Labrie F.,
RA Giguere V.;
RT "CIA, a novel estrogen receptor coactivator with a bifunctional
RT nuclear receptor interacting determinant.";
RL Mol. Cell. Biol. 21:343-353(2001).
RN [13]
RP PHOSPHORYLATION.
RX MEDLINE=95140025; PubMed=7838153;
RA Arnold S.F., Obourn J.D., Jaffe H., Notides A.C.;
RT "Serine 167 is the major estradiol-induced phosphorylation site on the
RT human estrogen receptor.";
RL Mol. Endocrinol. 8:1208-1214(1994).
RN [14]
RP PHOSPHORYLATION SITES SER-104 AND SER-106, AND MUTAGENESIS.
RX MEDLINE=99357754; PubMed=10428798;
RA Rogatsky I., Trowbridge J.M., Garabedian M.J.;
RT "Potentiation of human estrogen receptor alpha transcriptional
RT activation through phosphorylation of serines 104 and 106 by the
RT cyclin A-CDK2 complex.";
RL J. Biol. Chem. 274:22296-22302(1999).
RN [15]
RP STRUCTURE BY NMR OF 180-262.
RX MEDLINE=91061891; PubMed=2247153;
RA Schwabe J.W.E., Neuhaus D., Rhodes D.;
RT "Solution structure of the DNA-binding domain of the oestrogen
RT receptor.";
RL Nature 348:458-461(1990).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 180-262.
RX MEDLINE=94037103; PubMed=8221895;

RA Schwabe J.W.E., Chapman L., Finch J.T., Rhodes D.;
RT "The crystal structure of the estrogen receptor DNA-binding domain
RT bound to DNA: how receptors discriminate between their response
RT elements.";
RL Cell 75:567-578(1993).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF 305-548.
RX MEDLINE=97478539; PubMed=9338790;
RA Brzozowski A.M., Pike A.C.W., Dauter Z., Hubbard R.E., Bonn T.,
RA Engstrom O., Oehman L., Greene G.L., Gustafsson J.-A., Carlquist M.;
RT "Molecular basis of agonism and antagonism in the oestrogen
RT receptor.";
RL Nature 389:753-758(1997).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 306-544.
RX MEDLINE=98263297; PubMed=9600906;
RA Tanenbaum D.M., Wang Y., Williams S.P., Sigler P.B.;
RT "Crystallographic comparison of the estrogen and progesterone
RT receptor's ligand binding domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:5998-6003(1998).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (1.90 ANGSTROMS) OF 294-554.
RX MEDLINE=99091051; PubMed=9875847;
RA Shiau A.K., Barstad D., Loria P.M., Cheng L., Kushner P.J.,
RA Agard D.A., Greene G.L.;
RT "The structural basis of estrogen receptor/coactivator recognition and
RT the antagonism of this interaction by tamoxifen.";
RL Cell 95:927-937(1998).
RN [20]
RP 3D-STRUCTURE MODELING OF 311-547.
RX MEDLINE=98280806; PubMed=9619507;
RA Maalouf G.J., Xu W., Smith T., Mohr S.C.;
RT "Homology model for the ligand-binding domain of the human estrogen
RT receptor.";
RL J. Biomol. Struct. Dyn. 15:841-850(1998).
RN [21]
RP VARIANT VAL-400.
RX MEDLINE=90005402; PubMed=2792078;
RA Tora L., Mullick A., Metzger D., Ponglikitmongkol M., Park I.,
RA Chambon P.;
RT "The cloned human oestrogen receptor contains a mutation which alters
RT its hormone binding properties.";
RL EMBO J. 8:1981-1986(1989).
RN [22]
RP VARIANT ALA-447.
RX MEDLINE=92250650; PubMed=1577818;
RA Reese J.C., Katzenellenbogen B.S.;
RT "Characterization of a temperature-sensitive mutation in the hormone
RT binding domain of the human estrogen receptor. Studies in cell
RT extracts and intact cells and their implications for hormone-dependent
RT transcriptional activation.";
RL J. Biol. Chem. 267:9868-9873(1992).
RN [23]
RP VARIANT GLU-364.
RX MEDLINE=97120591; PubMed=8961262;
RA McInerney E.M., Ince B.A., Shapiro D.J., Katzenellenbogen B.S.;
RT "A transcriptionally active estrogen receptor mutant is a novel type
RT of dominant negative inhibitor of estrogen action.";
RL Mol. Endocrinol. 10:1519-1526(1996).
RN [24]
RP VARIANT CYS-160.
RX MEDLINE=97338667; PubMed=9195227;
RA Anderson T.I., Wooster R., Laake K., Collins N., Warren W., Skrede M.,
RA Eeles R., Tveit K.M., Johnston S.R.D., Dowsett M., Olsen A.O.,
RA Moeller P., Stratton M.R., Boerresen-Dale A.-L.;
RT "Screening for ESR mutations in breast and ovarian cancer patients.";
RL Hum. Mutat. 9:531-536(1997).
CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their
CC receptors are involved in the regulation of eukaryotic gene
CC expression and affect cellular proliferation and differentiation
CC in target tissues.
CC -!- SUBUNIT: Binds DNA as a homodimer. Binds UBE1C (By similarity).
CC Can form a heterodimer with ESR2. Interacts with NCOA3, NCOA5 and

CC NCOA6 coactivators, leading to a strong increase of transcription
 CC of target genes.

Query Match 98.1%; Score 1206.5; DB 1; Length 595;
 Best Local Similarity 96.3%; Pred. No. 1.8e-109;
 Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY	1	SLALSLTADQMV	SALLDAEPPILYSEYDPT	TRPFSEASMMGLLT	TNLADREL	VHMINWAKRV	60
Db	305	SLALSLTADQMV	SALLDAEPPILYSEYDPT	TRPFSEASMMGLLT	TNLADREL	VHMINWAKRV	364
QY	61	PGFVDLT	TLHDQVHLL	ECALWEILMIGLV	WRSMHPGKLL	FAPNLLDRNQK	CVGVMVEI 120
Db	365	PGFVDLT	TLHDQVHLL	ECALWEILMIGLV	WRSMHPGKLL	FAPNLLDRNQK	CVGVMVEI 424
QY	121	FDMLLATSSR	FRMMNLQGEFVCL	KSIIILLNSGVYTF	FXXXXXXXXXXX	EEKOHHRVLDKIT	180
Db	425	FDMLLATSSR	FRMMNLQGEFVCL	KSIIILLNSGVYTF	LSSTLKSLEEKOHHRVLDKIT	483	
QY	181	DTLIHLM	AKAGLT	TLQQQH	ORLAQLLLILSHIRH	MSNKGMEHLYSMCKKNVPLYDLLE	240
Db	484	DTLIHLM	AKAGLT	TLQQQH	ORLAQLLLILSHIRH	MSNKGMEHLYSMCKKNVPLYDLLE	543
QY	241	LDAHRL	246				
Db	544	LDAHRL	549				

RESULT 2

Q6QISS PRELIMINARY; PRT; 596 AA.

AC Q6QISS5;

DT 05-JUL-2004 (Tremblrel. 27, Created)

DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)

DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)

DE Estrogen receptor alpha.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Uterus;

RA Nishimura N., Tetsuka M.;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC !- SIMILARITY: Belongs to the nuclear hormone receptor family.

DR EMBL; AY538775; AAC46251.1; -

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR000536; Hmon_recept_lig.

DR InterPro; IPR001292; Oestrgn_receptor.

DR InterPro; IPR001723; Stdhrmn_receptor.

DR InterPro; IPR008946; Str_ncl_receptor.

DR InterPro; IPR001628; Znf_C4steroid.

DR Pfam; PF00104; Hormone_recep; 1.

DR Pfam; PF02159; Oest_recep; 1.

DR Pfam; PF00105; zf-C4; 1.

DR PRINTS; PR00543; OESTROGENR.

DR PRINTS; PR00398; STRDHORMONER.

DR PRINTS; PR00047; STROIDFINGER.

DR ProDom; PD000035; Znf_C4steroid; 1.

DR SMART; SM00430; HOLI; 1.

DR SMART; SM00399; Znf_C4; 1.

DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

DR DNA-binding; Metal-binding; Nuclear protein; Receptor;

KW Transcription regulation; Zinc; Zinc-finger.

SQ SEQUENCE 596 AA; 66489 MW; 3E2CE85BE7844FF2 CRC64;

DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
GN Name=Esrl; Synonyms=Nr3al, ESR, Estr, Estr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=91042558; PubMed=2484714;
RA White R., Lees J.A., Needham M., Ham J., Parker M.;
RT "Structural organization and expression of the mouse estrogen
RL receptor.";
RN Mol. Endocrinol. 1:735-744 (1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Bone, and Thymus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Takasaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Maekawa I., Osato N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Haezizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Sasaki D., Waterston R., Landers E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 50,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [3]
RP SEQUENCE OF 1-22 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20359284; PubMed=10899303;
RA Kos M., O'Brien S., Flouriot G., Gannon F.;
RT "Tissue-specific expression of multiple mRNA variants of the mouse
RL estrogen receptor alpha gene.";
RN FEBS Lett. 477:15-20 (2000).
RN [4]
RP SEQUENCE OF 269-599 FROM N.A.
RC STRAIN=SJL/J, and B10.S/J; TISSUE=Spleen;
RA Ma R.Z., Teuscher C.;
RT "Screening for candidate genes of mouse autoimmune diseases.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP CARBOHYDRATE-LINKAGE SITE SER-575.
RX MEDLINE=97153020; PubMed=8999954;
RA Jiang M.S., Hart G.W.;
RT "A subpopulation of estrogen receptors are modified by O-linked N-
RL acetylglucosamine.";
RN J. Biol. Chem. 272:2421-2428 (1997).
RN [6]
RP CARBOHYDRATE-LINKAGE SITES SER-10; THR-50 AND SER-575.
RX MEDLINE=21124487; PubMed=11226931;

RA Cheng X., Hart G.W.;
RT "Glycosylation of the murine estrogen receptor-alpha.";
RL J. Steroid Biochem. Mol. Biol. 75:147-158 (2000).
RN [7]
RP INTERACTION WITH NCOA3.
RX MEDLINE=97336097; PubMed=9192892;
RA Torchia J., Rose D.W., Inostroza J., Kamei Y., Westin S., Glass C.K.,
RA Rosenfeld M.G.;
RT "The transcriptional co-activator p/CIP binds CBP and mediates
RL nuclear-receptor function.";
RN Nature 387:677-684 (1997).
RN [8]
RP INTERACTION WITH NCOA6.
RX MEDLINE=20250907; PubMed=10788465;
RA Zhu Y.-J., Kan L., Qi C., Kanwar Y.S., Yeldandi A.V., Rao M.S.,
RA Reddy J.K.;
RT "Isolation and characterization of peroxisome proliferator-activated
RL receptor (PPAR) interacting protein (PRIP) as a coactivator for
RN PPAR.";
RN J. Biol. Chem. 275:13510-13516 (2000).
CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their
CC receptors are involved in the regulation of eukaryotic gene
CC expression and affect cellular proliferation and differentiation
CC in target tissues.
CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with
CC ESR2. Interacts with NCOA3 and NCOA6 coactivators, leading to a
CC strong increase of transcription of target genes. Interacts with
CC NCOA5. Binds UBE1C (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- PTM: Phosphorylated by cyclin A/CDK2 (By similarity).
CC -!- MISCELLANEOUS: In the absence of ligand, steroid hormone receptors
CC are thought to be weakly associated with nuclear components;
CC hormone binding greatly increases receptor affinity. The hormone-
CC receptor complex appears to recognize discrete DNA sequences
CC upstream of transcriptional start sites.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M38651; AAA37580.1; -.
DR EMBL; AK036627; BAC29510.1; -.
DR EMBL; AK041525; BAC30973.1; -.
DR EMBL; AJ276597; CAB85618.1; -.
DR EMBL; AF128221; AAF22562.1; -.
DR EMBL; AF128220; AAF22561.1; -.
DR PIR; A40061; QRMSE.
DR HSSP; P03372; IHCP.
DR TRANSFAC; T00259; -.
DR GlycoSuiteDB; P19785; -.
DR MGD; MGI:1352467; Esrl.
DR GO; GO:0016585; C:chromatin remodeling complex; ISS.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0016020; C:membrane; ISS.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0030284; F:estrogen receptor activity; ISS.
DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.
DR GO; GO:0016049; P:cell growth; NAS.
DR GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.
DR GO; GO:0045839; P:negative regulation of mitosis; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
DR InterPro; IPR000536; Hrmn_recept_lig.
DR InterPro; IPR001292; Oestrgn_receptor.
DR InterPro; IPR001723; Stdhrmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR

```
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF02159; Oest_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00543; OESTROGENR.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Glycoprotein; Nuclear protein; Phosphorylation; Receptor;
KW Steroid-binding; Transcription regulation; Zinc-finger.
FT DOMAIN 1 188 Modulating.
FT DNA_BIND 189 254 Nuclear receptor-type.
FT ZN_FING 189 209 C4-type.
FT ZN_FING 225 249 C4-type.
FT DOMAIN 255 314 Hinge.
FT DOMAIN 315 599 Steroid-binding.
FT DOMAIN 64 72 Poly-Ala.
FT MOD_RES 108 108 Phosphoserine (by CDK2) (By similarity).
FT MOD_RES 110 110 Phosphoserine (by CDK2) (By similarity).
FT MOD_RES 122 122 Phosphoserine (By similarity).
FT MOD_RES 171 171 Phosphoserine (by CK2) (By similarity).
FT MOD_RES 541 541 Phosphotyrosine (by Tyr-kinases) (By similarity).
FT CARBOHYD 10 10 O-linked (GlcNAc).
FT CARBOHYD 50 50 O-linked (GlcNAc).
FT CARBOHYD 575 575 O-linked (GlcNAc).
FT VARIANT 591 591 E -> Q (in strain SJL/J).
FT CONFLICT 269 269 L -> M (in Ref. 4).
SQ SEQUENCE 599 AA; 66955 MW; 05F5E2FC21CC0A8B CRC64;

Query Match 95.2%; Score 1171.5; DB 1; Length 599;
Best Local Similarity 93.1%; Pred. No. 4.9e-106;
Matches 229; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTFPFSEASMMGLLTNLADRELVMINWAKRV 60
Db 309 SPALSLTADQMVSAALLDAEPPMIYSEYDPTFPFSEASMMGLLTNLADRELVMINWAKRV 368

QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMVEI 120
Db 369 PGFGDLNLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMVEI 428

QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILNSGVYTFXXXXXXXKDHHRVLDKIT 180
Db 429 FDMLLATSSRRFRMNLQGEFVCLKSIILNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 487

QY 181 DTLIHLMAKAGLTQQQHQRLOAQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLLEM 240
Db 488 DTLIHLMAKAGLTQQQHRRRAQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLLEM 547

QY 241 LDAHRL 246
Db 548 LDAHRL 553

RESULT 5
ESR1_RAT STANDARD; PRT; 600 AA.
AC P06211;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
GN Name=Esrl; Synonyms=Nr3a1, Esr, Estr;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
```

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RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RA Muramatsu M.;
RL Submitted (MAR-1987) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87174780; PubMed=3031601;
RA Koike S., Sakai M.;
RT "Molecular cloning and characterization of rat estrogen receptor
RT CDNA.";
RL Nucleic Acids Res. 15:2499-2513(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Uterus;
RA Maggi A.M.A.;
RL Submitted (JUN-1991) to the EMBL/GenBank/DBJ databases.
RN [4]
RP INTERACTION WITH UBE1C.
RX PubMed=11818503;
RA Fan M., Long X., Bailey J.A., Reed C.A., Osborne E., Gize E.A.,
RA Kirk E.A., Bigsby R.M., Nephew K.P.;
RT "The activating enzyme of NEDD8 inhibits steroid receptor function.";
RL Mol. Endocrinol. 16:315-330(2002).
CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their
CC receptors are involved in the regulation of eukaryotic gene
CC expression and affect cellular proliferation and differentiation
CC in target tissues.
CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with
CC ESR2. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading
CC to a strong increase of transcription of target genes (By
CC similarity). Binds UBE1C.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- PTM: Phosphorylated by cyclin A/CDK2 (By similarity).
CC -!- MISCELLANEOUS: In the absence of ligand, steroid hormone receptors
CC are thought to be weakly associated with nuclear components;
CC hormone binding greatly increases receptor affinity. The hormone-
CC receptor complex appears to recognize discrete DNA sequences
CC upstream of transcriptional start sites.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y00102; CAA68287.1; -.
CC EMBL; X61098; CAA43411.1; -.
CC PIR; S07379; QRTE.
CC HSSP; P03372; IHCP.
CC TRANSFAC; T00258; -.
CC RGD; 2581; Esrl.
CC GO; GO:0016049; P:cell growth; ISS.
CC GO; GO:0045839; P:negative regulation of mitosis; ISS.
CC InterPro; IPR000536; Hrmn_recept_lig.
CC InterPro; IPR001292; Oestrn_receptor.
CC InterPro; IPR001723; Strhmn_receptor.
CC InterPro; IPR008946; Str_ncl_receptor.
CC InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00104; Hormone_recep; 1.
CC Pfam; PF02159; Oest_recep; 1.
CC Pfam; PF00105; zf-C4; 1.
CC PRINTS; PR00543; OESTROGENR.
CC PRINTS; PR00398; STRDHORMONER.
CC PRINTS; PR00047; STROIDFINGER.
CC ProDom; PD000035; Znf_C4steroid; 1.
CC SMART; SM00430; HOLI; 1.
CC SMART; SM00399; Znf_C4; 1.
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QY	61	PGFVDTLHDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVEGMVEI	121
DB	365	PGFLDSLHDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVEGMVEI	424
QY	121	FDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKXDHHRVLDKIT	180
DB	425	FDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKXDHHRVLDKIT	483
QY	181	DTLIHLMKAGLTLOQOQHQRLLAQLLILSHIRHMSNKGMEHLYSMCKKNVVPDYDLLLEM	240
DB	484	DTLIHLMKAGLTLOQOQHRRLLAQLLILSHFRHMSNKGMEHLYNMCKKNVVPDYDLLLEM	543
QY	241	LDAHRL 246	
DB	544	LDAHRL 549	

RESULT 7

ESR1 MESAU STANDARD; PRT; 595 AA.

AC Q9QZJ5; Q9QZG6;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE -Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).

GN Name=ESR1; Synonyms=NR3A1, ESR;

OS Mesocricetus auratus (Golden hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

OC Mesocricetus.

OX NCBI_TaxID=10036;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Uterus;

RX MEDLINE=20197937; PubMed=10731637;

RA Bhat H.K., Vadgama J.V.;

RT "Hamster estrogen receptor cDNA: cloning and mRNA expression.";

RL J. Steroid Biochem. Mol. Biol. 72:47-53(2000).

RN [2]

RP SEQUENCE OF 98-291 FROM N.A.

RA Jones J.E., Carpenter C.D., Lubbers L.S., Petersen S.L., Wade G.N.;

RT "Return of lordosis after food deprivation and refeeding in Syrian hamsters.";

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues (By similarity).

CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ESR2. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading to a strong increase of transcription of target genes. Binds UBE1C (By similarity).

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.

CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3 subfamily.

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EMBL; AF181077; AAD53956.1; -.

EMBL; AF184276; AAF02721.1; -.

DR HSSP; P03372; 1HCQ.

DR GO; GO:0016585; C:chromatin remodeling complex; ISS.

DR GO; GO:0016020; C:membrane; ISS.

DR GO; GO:0030284; F:estrogen receptor activity; ISS.

SQ SEQUENCE 594 AA; 66103 MW; DD36CA7C24C74B95 CRC64;
Query Match 93.2%; Score 1146; DB 1; Length 594;
Best Local Similarity 91.5%; Pred. No. 1.5e-103;
Matches 225; Conservative 7; Mismatches 12; Indels 2; Gaps 2;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SPVLSLTAEQMISALLDAEPPVLYSEYDATRPFNEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 120
Db 365 PGFVDLSLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 424
QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 180
Db 425 FDMLLATSSRLRMNMLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483
QY 181 DTLIHLMAGLTLQQHQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEM 240
Db 484 DTLIHLMAGLTL-QQHRRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEM 542
QY 241 LDAHRL 246
Db 543 LDAHRL 548

RESULT 10
ESR1_POEGU STANDARD; PRT; 587 AA.
AC Q91250;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
GN Name=ESR1; Synonyms=NR3A1, ESR;
OS Poephila guttata (Zebra finch) (Taeniopygia guttata).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;
OC Estrildinae; Taeniopygia.
OX NCBI_TaxID=59729;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX MEDLINE=97163508; PubMed=9010328;
RA Jacobs E.C., Arnold A.P., Campagnoni A.T.;
RT "Zebra finch estrogen receptor cDNA: cloning and mRNA expression.";
RL "Zebra finch estrogen receptor cDNA: cloning and mRNA expression.";
CC !- FUNCTION: The steroid hormones and their receptors are involved in
CC the regulation of eukaryotic gene expression and affect cellular
CC proliferation and differentiation in target tissues.
CC !- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ER-
CC beta (By similarity).
CC !- SUBCELLULAR LOCATION: Nuclear.
CC !- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC !- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L79911; AAB81108.1; -.
DR HSSP; P03372; IHCP.
DR GO; GO:0016585; C:chromatin remodeling complex; ISS.
DR GO; GO:0016020; C:membrane; ISS.
DR GO; GO:0030284; F:estrogen receptor activity; ISS.
DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.

DR GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
DR InterPro; IPR00536; Hmon_recept_lig.
DR InterPro; IPR001292; Oestrgn_receptor.
DR InterPro; IPR001723; Stdhrmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF02159; Oest_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00543; OESTROGENR.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Steroid-binding;
KW Transcription regulation; Zinc-finger.
FT DOMAIN 1 176 Modulating.
FT DNA_BIND 177 242 Nuclear receptor-type.
FT ZN_FING 177 197 C4-type.
FT ZN_FING 213 237 C4-type.
FT DOMAIN 243 302 Hinge.
FT DOMAIN 303 587 Steroid-binding.
SQ SEQUENCE 587 AA; 66553 MW; 2B254168A7A910AB CRC64;
Query Match 93.0%; Score 1144.5; DB 1; Length 587;
Best Local Similarity 90.2%; Pred. No. 2.1e-103;
Matches 222; Conservative 12; Mismatches 11; Indels 1; Gaps 1;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 297 SPALSLTAEQMVSAALLAEAPLVSEYDPTNRPFNEASMTLLTNLADRELVHMINWAKRV 356
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 120
Db 357 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 416
QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 180
Db 417 FDMLLATAARFRMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 475
QY 181 DTLIHLMAGLTLQQHQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEM 240
Db 476 DTLIHLMAGLTLQQHQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEM 535
QY 241 LDAHRL 246
Db 536 LDAHRL 541

RESULT 11
ESR1_CHICK STANDARD; PRT; 589 AA.
ID ESR1_CHICK
AC P06212;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
GN Name=ESR1; Synonyms=NR3A1, ESR;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86247578; PubMed=3755102;
RA Krust A., Green S., Argos P., Kumar V., Walter P., Bornert J.-M.,
RA Chambon P.;
RT "The chicken oestrogen receptor sequence: homology with v-erba and the
human oestrogen and glucocorticoid receptors.";

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OM protein - protein search, using sw model

Run on: November 8, 2004, 08:14:27 ; Search time 12.049 Seconds
(without alignments)
1964.426 Million cell updates/sec

Title: US-09-830-693B-28
Perfect score: 1230
Sequence: 1 SLALSLTADQMVSALLDAEP.....CKNVVPLYDLLLEMLDAHRL 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1197.5	97.4	595	1 QRHUE	estrogen receptor
2	1171.5	95.2	599	1 QRMSE	estrogen receptor
3	1167.5	94.9	600	1 QRRTE	estrogen receptor
4	1164.5	94.7	595	2 I47140	estradiol receptor
5	1145.5	93.1	701	2 S64737	80K estrogen recep
6	1143.5	93.0	589	1 QRCHE	estrogen receptor
7	1037.5	84.3	586	1 QRXLE	estrogen receptor
8	792.5	64.4	620	2 T10423	estrogen receptor
9	781.5	63.5	535	2 S58224	estrogen receptor
10	764.5	62.2	477	2 S71400	estrogen receptor
11	764.5	62.2	530	2 JC5939	estrogen receptor
12	758.5	61.7	574	2 A37197	estrogen receptor
13	750.5	61.0	503	2 JW0046	estrogen receptor
14	626.5	50.9	133	2 S26595	estrogen receptor
15	547.5	44.5	121	2 I67419	estradiol receptor
16	374.5	30.4	433	2 B29345	steroid hormone re
17	354.5	28.8	433	2 S58087	estrogen receptor
18	323	26.3	521	2 A29345	steroid hormone re
19	263.5	21.4	758	2 S60586	glucocorticoid rec
20	248	20.2	930	2 A25923	progesterone recep
21	248	20.2	933	1 QRHUP	progesterone recep
22	247	20.1	923	2 A39596	progesterone recep
23	246	20.0	923	2 I53280	progesterone recep
24	243.5	19.8	467	2 A43781	retinoid-X-recepto
25	243	19.8	786	2 A35466	progesterone recep
26	241.5	19.6	488	2 C41977	retinoid receptor
27	240	19.5	441	2 I50515	retinoid X recepto
28	238.5	19.4	771	2 A54273	glucocorticoid rec
29	236.5	19.2	462	1 S09592	retinoid X recepto

30	236	19.2	467	2 S26668	retinoic acid rece
31	236	19.2	467	2 A47278	retinoid X recepto
32	234.5	19.1	463	2 S26670	retinoic acid rece
33	234.5	19.1	463	2 B41727	retinoid-X recepto
34	233.5	19.0	470	2 D41977	retinoid receptor
35	230.5	18.7	777	1 QRHUGA	glucocorticoid rec
36	230.5	18.7	783	1 A25691	glucocorticoid rec
37	229.5	18.7	742	1 QRHUGB	glucocorticoid rec
38	227.5	18.5	379	2 I50514	retinoid X recepto
39	224.5	18.3	848	2 JG0194	androgen receptor
40	223	18.1	533	2 S37781	retinoid X recepto
41	222	18.0	410	2 S26669	retinoic acid rece
42	222	18.0	446	2 A34418	H-2 region II bind
43	222	18.0	448	2 D41727	retinoid X recepto
44	222	18.0	451	2 A41651	retinoic acid rece
45	222	18.0	520	2 I84718	RXR-beta1 isoform

ALIGNMENTS

RESULT 1

QRHUE

estrogen receptor 1 - human
N;Alternate names: ERL; estrogen receptor alpha
C;Species: Homo sapiens (man)
C;Date: 28-May-1986 #sequence revision 28-May-1986 #text change 09-Jul-2004
C;Accession: A94284; A93376; A43021; S27143; S34000; A41925; A03244; C41925; D41
R;Greene, G.L.; Gilna, P.; Waterfield, M.; Baker, A.; Hort, Y.; Shine, J.
Science 231, 1150-1154, 1986
A;Title: Sequence and expression of human estrogen receptor complementary DNA.
A;Reference number: A94284; MUID:86122927; PMID:3753802
A;Accession: A94284
A;Molecule type: mRNA
A;Residues: 1-595 <GR1>
A;Cross-references: UNIPROT:Q14268; UNIPROT:Q9UE35; GB:M12674; NID:g182192; PIDN:AAA5239
R;Green, S.; Walter, P.; Kumar, V.; Krust, A.; Bornert, J.M.; Argos, P.; Chambon, P.
Nature 320, 134-139, 1986
A;Title: Human oestrogen receptor cDNA: sequence, expression and homology to v-erb-A.
A;Reference number: A93376; MUID:86146892; PMID:3754034
A;Accession: A93376
A;Molecule type: mRNA
A;Residues: 1-595 <GR2>
A;Cross-references: GB:X03635; NID:g31233; PIDN:CAA27284.1; PID:g31234
R;Ponglikitmongkol, M.; Green, S.; Chambon, P.
EMBO J. 7, 3385-3388, 1988
A;Title: Genomic organization of the human oestrogen receptor gene.
A;Reference number: A43021; MUID:89091079; PMID:3145193
A;Accession: A43021
A;Molecule type: DNA
A;Residues: 143-161;205-225;244-264;356-374,'G',376;402-422;447-460,'P',462-467;508-528
R;Keaveney, M.; Klug, J.; Gannon, F.
DNA Seq. 2, 347-358, 1992
A;Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene
A;Reference number: S27140; MUID:93075998; PMID:1476547
A;Accession: S27143
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-115 <KEA>
A;Cross-references: EMBL:X62462; NID:g31201; PIDN:CAA44322.1; PID:g31205
R;Pfeffer, U.; Fecarotta, B.; Castagnetta, L.; Vidali, G.
Cancer Res. 53, 741-743, 1993
A;Title: Estrogen receptor variant messenger RNA lacking exon 4 in estrogen-responsive h
A;Reference number: S34000; MUID:93153765; PMID:7916651
A;Accession: S34000
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 216-254,367-399,'G',401-434 <PRE>
A;Cross-references: EMBL:X73067; NID:g579865; PIDN:CAA51528.1; PID:g939886
A;Note: the authors translated the codon GGG for residue 400 as Val
R;Dotzlaw, H.; Alkhalaf, M.; Murphy, L.C.
Mol. Endocrinol. 6, 773-785, 1992
A;Title: Characterization of estrogen receptor variant mRNAs from human breast cancers.

A;Reference number: A41925; MUID:92293154; PMID:1603086
A;Accession: A41925
A;Molecule type: mRNA
A;Residues: 1-214,'ELPTLC' <DOT>
A;Cross-references: GB:M69297; NID:g182218; PIDN:AAA58462.1; PID:g182219
A;Experimental source: clone 4; breast cancer
A;Note: sequence has been revised after extraction from NCBI backbone
A;Note: the complete sequence of neither the nucleotide nor the protein is shown in this
A;Note: sequence extracted from NCBI backbone (NCBIN:106580)
A;Accession: B41925
A;Status: significant sequence differences
A;Molecule type: mRNA
A;Cross-references: GB:M69296
A;Experimental source: clone 24; breast cancer
A;Note: sequence extracted from NCBI backbone (NCBIN:106597)
C;Comment: The steroid hormones and their receptors are involved in the regulation of eu
C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
complex appears to recognize discrete DNA sequences upstream of transcriptional start sit
C;Genetics:
A;C; GDB:ESR1; ESR
A;Cross-references: GDB:119120; OMIM:133430.
A;Map position: 6q25.1-6q25.1
A;Introns: 151/2; 215/1; 254/1; 366/1; 412/2; 457/1; 518/2
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid hormone receptor; transcriptio
F;1-120/Domain: amino-terminal <NH2>
F;121-299/Domain: DNA binding #status predicted <DNA>
F;183-456/Domain: erba transforming protein homology <ERBA>
F;185-205/Region: zinc finger CCCC motif
F;221-245/Region: zinc finger CCCC motif
F;300-595/Domain: steroid binding #status predicted <STB>
F;236,305/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 97.4%; Score 1197.5; DB 1; Length 595;
Best Local Similarity 95.9%; Pred. No. 5.3e-111;
Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFFSEASMMGLLTNLADRELVHMINWAKRV 364

Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCKVEGMVEI 120
Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPVKLLFAPNLLDRNQKCKVEGMVEI 424

Qy 121 FDMLLATSSRRFRMMNLQGEFEVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db 425 FDMLLATSSRRFRMMNLQGEFEVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483

Qy 181 DTLIHLMAKAGLTLOQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEEM 240
Db 484 DTLIHLMAKAGLTLOQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEEM 543

Qy 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 2
QRMSE
estrogen receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: A40061
R;White, R.; Lees, J.A.; Needham, M.; Ham, J.; Parker, M.
Mol. Endocrinol. 1, 735-744, 1987
A;Title: Structural organization and expression of the mouse estrogen receptor.
A;Reference number: A40061; MUID:91042558; PMID:2484714
A;Accession: A40061
A;Molecule type: mRNA
A;Residues: 1-599 <WHI>
A;Cross-references: UNIPROT:P19785; GB:M38651; NID:g193179; PIDN:AAA37580.1; PID:g193180
C;Comment: The steroid hormones and their receptors are involved in the regulation of eu

C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
complex appears to recognize discrete DNA sequences upstream of transcriptional start site
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recept
F;1-183/Domain: amino-terminal <NH2>
F;184-275/Domain: DNA binding #status predicted <DNA>
F;187-460/Domain: erba transforming protein homology <ERBA>
F;187-210/Region: zinc finger CCCC motif
F;223-245/Region: zinc finger CCCC motif
F;260-275/Region: nuclear location signal
F;304-556/Domain: steroid binding #status predicted <STB>
F;189,192,206,209/Binding site: zinc (Cys) #status predicted
F;225,231,241,244/Binding site: zinc (Cys) #status predicted
F;240,309/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 95.2%; Score 1171.5; DB 1; Length 599;
Best Local Similarity 93.1%; Pred. No. 2.1e-108;
Matches 229; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 309 SPALSLTADQMVSALLDAEPPMIYSEYDPSRPFSEASMMGLLTNLADRELVHMINWAKRV 368

Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCKVEGMVEI 120
Db 369 PGFGDLNLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCKVEGMVEI 428

Qy 121 FDMLLATSSRRFRMMNLQGEFEVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db 429 FDMLLATSSRRFRMMNLQGEFEVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 487

Qy 181 DTLIHLMAKAGLTLOQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEEM 240
Db 488 DTLIHLMAKAGLTLOQQHRRLAQLLLILSHIRHMSNKGMEHLYNMKCKNVVPLYDLLEEM 547

Qy 241 LDAHRL 246
Db 548 LDAHRL 553

RESULT 3
QRRTE
estrogen receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: S07379; S16731
R;Koike, S.; Sakai, M.; Muramatsu, M.
Nucleic Acids Res. 15, 2499-2513, 1987
A;Title: Molecular cloning and characterization of rat estrogen receptor cDNA.
A;Reference number: S07379; MUID:87174780; PMID:3031601
A;Accession: S07379
A;Molecule type: mRNA
A;Residues: 1-600 <KOI>
A;Cross-references: UNIPROT:P06211; EMBL:Y00102; NID:g56110; PIDN:CAA68287.1; PID:g56111
R;Maggi, A.M.A.
submitted to the EMBL Data Library, June 1991
A;Reference number: S16731
A;Accession: S16731
A;Molecule type: mRNA
A;Residues: 1-487,'T',489-600 <MAG>
A;Cross-references: EMBL:X61098; NID:g56120; PIDN:CAA43411.1; PID:g56121
C;Comment: The steroid hormones and their receptors are involved in the regulation of eu
C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
complex appears to recognize discrete DNA sequences upstream of transcriptional start site
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recept
F;1-184/Domain: amino-terminal <NH2>
F;185-276/Domain: DNA binding #status predicted <DNA>
F;188-461/Domain: erba transforming protein homology <ERBA>
F;188-211/Region: zinc finger CCCC motif
F;224-246/Region: zinc finger CCCC motif
F;261-276/Region: nuclear location signal
F;305-557/Domain: steroid binding #status predicted <STB>

F;190,193,207,210/Binding site: zinc (Cys) #status predicted
F;226,232,242,245/Binding site: zinc (Cys) #status predicted
F;241,310/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match	94.9%	Score 1167.5;	DB 1;	Length 600;
Best Local Similarity	92.7%	Pred. No. 5.2e-108;		
Matches 228; Conservative	5;	Mismatches 12;	Indels 1;	Gaps 1;

Qy	1	SL	SL	TADQ	VS	ALLD	AE	PI	LY	SEYD	PT	TR	PF	SE	AS	MM	GL	LT	NL	AD	RE	LH	MI	NW	AK	RV	60	
Db	310	SP	AL	SL	TADQ <td>VS</td> <td>ALLD <td>AE <td>PI <td>LY <td>SEYD <td>PT <td>TR <td>PF <td>SE <td>AS <td>MM <td>GL <td>LT <td>NL <td>AD <td>RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	VS	ALLD <td>AE <td>PI <td>LY <td>SEYD <td>PT <td>TR <td>PF <td>SE <td>AS <td>MM <td>GL <td>LT <td>NL <td>AD <td>RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	AE <td>PI <td>LY <td>SEYD <td>PT <td>TR <td>PF <td>SE <td>AS <td>MM <td>GL <td>LT <td>NL <td>AD <td>RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	PI <td>LY <td>SEYD <td>PT <td>TR <td>PF <td>SE <td>AS <td>MM <td>GL <td>LT <td>NL <td>AD <td>RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	LY <td>SEYD <td>PT <td>TR <td>PF <td>SE <td>AS <td>MM <td>GL <td>LT <td>NL <td>AD <td>RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	SEYD <td>PT <td>TR <td>PF <td>SE <td>AS <td>MM <td>GL <td>LT <td>NL <td>AD <td>RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	PT <td>TR <td>PF <td>SE <td>AS <td>MM <td>GL <td>LT <td>NL <td>AD <td>RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	TR <td>PF <td>SE <td>AS <td>MM <td>GL <td>LT <td>NL <td>AD <td>RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td>	PF <td>SE <td>AS <td>MM <td>GL <td>LT <td>NL <td>AD <td>RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td></td></td></td></td></td></td></td></td>	SE <td>AS <td>MM <td>GL <td>LT <td>NL <td>AD <td>RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td></td></td></td></td></td></td></td>	AS <td>MM <td>GL <td>LT <td>NL <td>AD <td>RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td></td></td></td></td></td></td>	MM <td>GL <td>LT <td>NL <td>AD <td>RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td></td></td></td></td></td>	GL <td>LT <td>NL <td>AD <td>RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td></td></td></td></td>	LT <td>NL <td>AD <td>RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td></td></td></td>	NL <td>AD <td>RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td></td></td>	AD <td>RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td></td>	RE <td>LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td></td>	LH <td>MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td></td>	MI <td>NW <td>AK <td>RV <td>369</td> </td></td></td>	NW <td>AK <td>RV <td>369</td> </td></td>	AK <td>RV <td>369</td> </td>	RV <td>369</td>	369

[illegible]

Qy	121	FDMLLATSSRRFRMNLQGEFFVCLKSIILLNSGVYTFXXXXXXXEEKHHRVLDKIT	180
Db	430	FDMLLATSSRRFRMNLQGEFFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIN	488

D_b DTLIHLMAKAGLTQQQHQRLAQLLLILSHIRMSNKGMEHLYSMCKKNVPLYDLLLEM 240
|||||:|||||:|||||:|||||:|||||:
Qy DTLIHLMAKAGLTQQQHQRLAQLLLILSHIRMSNKGMEHLYSMCKKNVPLYDLLLEM 240

Qy	241	LDAHRL	246
Db	549	LDAHRL	554

RESULT 4
I47140
estradiol receptor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I47140; S66250; S32402
R:Bokenkamp, D.; Jungblut, P.W.; Thole, H.H.
Mol. Cell. Endocrinol. 104, 163-172, 1994
A:Title: The C-terminal half of the porcine estradiol receptor contains no post-translational
A:Reference number: I47140; MUID:95080454; PMID:7988744
A:Accession: I47140
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-595 <BOX>

A: Cross-references: UNIPROT:Q29040; EMBL:Z37167; NID:G587554; PIDN:CAA85524.1; PID:G587554
A: Experimental source: uterus
R: Thole, H.H.; Maschler, I.; Jungblut, P.W.
Eur. J. Biochem. 231, 510-516, 1995
A: Title: Surface mapping of the ligand-filled C-terminal half of the porcine estradiol receptor
A: Reference number: S66250; MUID:95361877; PMID:7635163
A: Accession: S66250

A: Molecule type: protein
A: Residues: 297-307; 310-313; 320-323; 329-332; 337-340; 417-420; 466-473 <THO>
A: Experimental source: uterus
R: Thole, H.H.

FEBS Lett. 320, 92-96, 1993
A;Title: Assignment of the ligand binding site of the porcine estradiol receptor to the
A;Reference number: S32402; MUID:93209384; PMID:8458437
A;Accession: S32402

A;Molecule type: protein
A;Residues: 303-323 <THW>
C;Superfamily: estrogen receptor; erbA transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid hormone receptor; transcription factor
F;1-120/Domain: amino-terminal <NH2>

F;121-299/Domain: DNA binding #status predicted <DNA>
 F;183-456/Domain: erba transforming protein homology <ERBA>
 F;185-205/Region: zinc finger CCCC motif
 F;221-245/Region: zinc finger CCCC motif
 F;256-271/Region: nuclear location signal
 F;300-595/Domain: steroid binding #status predicted <STB>
 F;185,188,202,205/Binding site: zinc (Cys) #status predicted
 F;221,227,237,240/Binding site: zinc (Cys) #status predicted
 F;236,305/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 94.7%; Score 1164.5; DB 2; Length 595;
Best Local Similarity 91.9%; Pred. No. 1e-107;
Matches 226; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY	1	SLALSLTADQMVSALLDAPPIIYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRV	60
Dd	305	SPVLSTLTDQMISALLEABPPIIYSEYDPTTRPLSEASMMGLLTNLADRELVHMINWAKRV	364

Qy	61	PGFVDLTLLHDQVHLLLECAWLEILMIGLVWRSMEH PGLLFAPNLLLDNRNQKCVEGMVEI	120
Db	365	PGFLDLSLHDQVHLLLECAWLEILMIGLVWRSMEH PGLLFAPNLLLDNRNQKCVEGMVEI	424

QY	121	FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT	180
Db	425	FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT	483

Qy	181	DTLIHLMAKAGLT	TLQOQ	QRLAQL	LLIL	LSHIRHMS	NKGM	EHL	YSNM	CKNV	VPLY	DLL	LEM	240
				:				:						
D _b	484	DTLIHLMAKAGLT <th>TLQOQ</th> <th>HRRLAQL</th> <th>LLIL</th> <th>LSHFRHMS</th> <th>NKGM</th> <th>EHL</th> <th>YSNM</th> <th>CKNV</th> <th>VPLY</th> <th>DLL</th> <th>LEM</th> <th>543</th>	TLQOQ	HRRLAQL	LLIL	LSHFRHMS	NKGM	EHL	YSNM	CKNV	VPLY	DLL	LEM	543

Qy 241 LDAHRL 246
|||
Db 544 LDAHRL 549

RESULT 5
S64737
80K estrogen receptor - human
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C:Accession: S64737
R:Pink, J.J.; Wu, S.Q.; Wolf, D.M.; Billimoria, M.M.; Jordan, V.C.
Nucleic Acids Res. 24, 962-969, 1996
A:Title: A novel 80 kDa human estrogen receptor containing a duplication of exons 6 and
A:Reference number: S64737; MUID:96174665; PMID:8600466
A:Accession: S64737
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-701 <PIN>
A:Cross-references: EMBL:U47678; NID:g1197854; PIDN:AAB00115.1; PID:g1197855
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
C:Superfamily: estrogen receptor; erba transforming protein homology
C:Keywords: steroid hormone receptor; zinc finger
F:183-456/Domain: erba transforming protein homology <ERBA>
F:518-562/Domain: erba transforming protein homology #status atypical <ERB2>

Query Match 93.1%; Score 1145.5; DB 2; Length 701;
Best Local Similarity 67.2%; Pred. NO. 9.7e-106;
Matches 236; Conservative 0; Mismatches 10; Indels 105; Gaps 1;

[illegible][illegible]

QY	121	FDMLLATSRPRMNLQGEFVCLKSIILLNSGVYTFXX	-----	159
Dp	425	FDMLLATSRPRMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDTHRVLDKITD	-----	484

Qy	160	-----	159
Db	485	TLIHIMAKAGITLOOCHORIAOLILITLSHTRHMENOGKCVEGMVEIFDMIATSSRFMM	544

Oy	160	-----XXXXXXXXXXEEDKHVRVLDKITDTTLIHLMAKAGLTQ	195
Dh	545	NLOGEFFVCIKSITIIINSGIWTEFSSTIKSIFEKDHTHPVI	504
		DKITDTTILHLMACAGLTQ	

Qy	196	QQHQLAQLLLILSHIRMSNKGNEHLYSMKCKNVVPLYDLLLLLEMLDAHRL	246
D _b	605	QQHQLAQLLLILSHIRMSNKGNEHLYSMKCKNVVPLYDLLLLLEMLDAHRL	655

RESULT 6
QRCHE
estrogen receptor - chicken
C;Species: Gallus gallus (Chicken)
C;Date: 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: A40914; S07192
R;Maxwell, B.L.; McDonnell, D.P.; Conneely, O.M.; Schulz, T.Z.; Greene, G.L.; O'Malley, M.L. Endocrinol. 1, 25-35, 1987
A;Title: Structural organization and regulation of the chicken estrogen receptor.
A;Reference number: A40914; MUID:88318621; PMID:2901032
A;Accession: A40914
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-589 <MAX>
A;Cross-references: UNIPROT:P06212
R;Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P. EMBO J. 5, 891-897, 1986
A;Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human oes
A;Reference number: S07192; MUID:86247578; PMID:3755102
A;Accession: S07192
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-256, E', 258-589 <KRU>
A;Cross-references: EMBL:X03805; NID:g63378; PIDN:CAA27433.1; PID:g63380
C;Comment: The steroid hormones and their receptors are involved in the regulation of eu
C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
complex appears to recognize discrete DNA sequences upstream of transcriptional start sit
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep
F;1-173/Domain: amino-terminal <NH2>
F;174-265/Domain: DNA binding #status predicted <DNA>
F;177-450/Domain: erba transforming protein homology <ERBA>
F;177-200/Region: zinc finger CCCC motif
F;213-235/Region: zinc finger CCCC motif
F;250-265/Region: nuclear location signal
F;294-546/Domain: steroid binding #status predicted <STB>
F;179,182,196,199/Binding site: zinc (Cys) #status predicted
F;215,221,231,234/Binding site: zinc (Cys) #status predicted
F;230,299/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 93.0%; Score 1143.5; DB 1; Length 589;
Best Local Similarity 90.2%; Pred. No. 1.2e-105;
Matches 222; Conservative 12; Mismatches 11; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 299 SPALSLTAEQMVSAALLAEPPIVYSEYDPNRPFPNEASMMTLLTNLADRELVHMINWAKRV 358

Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGVMVEI 120
Db 359 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGVMVEI 418

Qy 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db 419 FDMLLATAARFRMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEERDYIHRVLDKIT 477

Qy 181 DTLIHLMAKAGLTLOQQHORLAQLLLILSHIRHMSNKGMEHLYSMCKKNVPLYDLLLEM 240
Db 478 DTLIHLMAKSGLSLQQQRRRLAQLLLILSHIRHMSNKGMEHLYNMCKKNVPLYDLLLEM 537

Qy 241 LDAHRL 246
Db 538 LDAHRL 543

RESULT 7
QRCLE
estrogen receptor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 28-Feb-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: A40907

R;Weiler, I.J.; Lew, D.; Shapiro, D.J. Mol. Endocrinol. 1, 355-362, 1987
A;Title: The Xenopus laevis estrogen receptor: sequence homology with human and avian rec
A;Reference number: A40907; MUID:90331927; PMID:3274894
A;Accession: A40907
A;Molecule type: mRNA
A;Residues: 1-586 <WEI>
A;Cross-references: UNIPROT:P81559; GB:L20735
C;Comment: The steroid hormones and their receptors are involved in the regulation of eu
C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
omplex appears to recognize discrete DNA sequences upstream of transcriptional start site
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep
F;1-174/Domain: amino-terminal <NH2>
F;175-266/Domain: DNA binding #status predicted <DNA>
F;178-448/Domain: erba transforming protein homology <ERBA>
F;178-201/Region: zinc finger CCCC motif
F;214-237/Region: zinc finger CCCC motif
F;251-266/Region: nuclear location signal
F;292-544/Domain: steroid binding #status predicted <STB>
F;180,183,197,200/Binding site: zinc (Cys) #status predicted
F;216,222,232,235/Binding site: zinc (Cys) #status predicted
F;231/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 84.3%; Score 1037.5; DB 1; Length 586;
Best Local Similarity 80.1%; Pred. No. 4.3e-95;
Matches 197; Conservative 25; Mismatches 23; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 297 SPVLSLTAEQLISALMEAEAPIVSEHDS TKPLSEASMMTLLTNLADRELVHMINWAKRV 356

Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGVMVEI 120
Db 357 PGFVDLTLDQVHLLCAWLEILMVGLIWRSVHPGKLSFAPNLLDRNQRCVEGLVEI 416

Qy 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db 417 FDMLVTTATRRFRMMLRGEEFICLSIILLNSGVYTF-LSSTLESLEDTDLIHILDKII 475

Qy 181 DTLIHLMAKAGLTLOQQHORLAQLLLILSHIRHMSNKGMEHLYSMCKKNVPLYDLLLEM 240
Db 476 DTLVHFMAKSGLSLQQQRRRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVPLYDLLLEM 535

Qy 241 LDAHRL 246
Db 536 LDAHRI 541

RESULT 8
T10423
estrogen receptor - Oryzias sp. (strain d-rR)
C;Species: Oryzias sp.
A;Variety: strain d-rR
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T10423
R;Okada, H.; Kawahara, T.; Yamashita, I. submitted to the EMBL Data Library, March 1994
A;Description: Cloning of medaka estrogen receptor cDNA.
A;Reference number: Z17013
A;Accession: T10423
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-620 <OKA>
A;Cross-references: UNIPROT:P50241; EMBL:D28954
A;Experimental source: strain d-rR, liver
C;Genetics:
A;Gene: MER
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation
F;184-460/Domain: erba transforming protein homology <ERB>

Query Match 64.4%; Score 792.5; DB 2; Length 620;

Best Local Similarity 63.0%; Pred. No. 1.1e-70;		
Matches 155;	Conservative 39;	Mismatches 43; Indels 9; Gaps 2;
QY	5	SLTADQMVSALLDAEPPILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFV 64
Db	313	SIPPEQVLLLLQGAEPPICSRQKLSRPYTEVTMTLLTSMADKELVHMIWAKKLPGL 372
QY	65	DLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEIFDML 124
Db	373	QLSLHDQVLLLESSWLEVMIGLIWRSIHCPGKLIFAQDLILDNRNEGDCVEGTEIFDML 432
QY	125	LATSSRFRMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDH----IHRVLDKIT 180
Db	433	LATASRFRVLKPEEFVCLKAIILLNSGAFSCTGTM-----EPLHNSAAVQSMLDTIT 487
QY	181	DTLIHLMAKAGLTQQQHQRLAQLLILSHIRHMSNKGMEHLYSMCKCNVPLYDLLLEM. 240
Db	488	DALIHYSISQGYLAQEARRQAQLLLLLSHIRHMSNKGMEHLYSMCKCNKVPPLYDLLLEM 547
QY	241	LDAHRL 246
Db	548	LDAHRL 553

RESULT 9
S58224
oestrogen receptor - Atlantic salmon (fragment)
C/Species: Salmo salar (Atlantic salmon)
C/Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C/Accession: S58224
R/Rogers, S.A.; Llewellyn, L.; Ramsurn, V.P.; Sweeney, G.E.; Wigham, T.
submitted to the EMBL Data Library, July 1995
A/Reference number: S58224
A/Accession: S58224
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-535 <ROG>
A/Cross-references: UNIPROT:P50242; EMBL:X89959; NID:G929901; PIDN:CAA61999.1; PID:G92999.1
C/Superfamily: estrogen receptor; erba transforming protein homology
C/Keywords: steroid hormone receptor; zinc finger
F/103-382/Domain: erba transforming protein homology <ERBA>

Query Match	63.5%;	Score	781.5;	DB 2;	Length	535;			
Best Local Similarity	61.7%;	Pred.	No. 1.1e-69;						
Matches	150;	Conservative	39;	Mismatches	53;	Indels	1;	Gaps	1;

QY	4	L	S	L	T	A	D	Q	M	V	S	A	L	L	D	A	E	P	I	L	S	E	Y	D	P	T	R	P	F	E	A	S	M	G	L	T	N	L	A	D	R	E	L	V	H	M	I	N	A	K	R	V	P	G	F	63			
DB	234	I	T	M	P	E	Q	V	L	F	L	L	Q	A	E	P	A	L	C	S	R	Q	V	A	R	P	Y	T	E	V	T	M	T	L	T	S	M	A	D	K	E	L	V	H	M	I	A	N	A	K	V	P	G	F	293				
QY	64	V	D	L	T	L	H	D	Q	V	H	L	E	C	A	W	L	E	I	M	I	G	L	V	W	R	S	M	E	H	P	G	K	L	L	P	A	P	N	L	L	D	R	N	O	G	K	C	V	E	G	M	V	E	I	F	D	M	123
DB	294	O	E	L	S	L	H	D	Q	V	L	E	S	S	W	L	E	V	M	I	G	L	I	W	R	S	I	H	C	P	G	K	L	I	F	A	Q	D	L	I	D	R	S	E	G	D	C	V	E	G	M	A	I	F	D	M	353		
QY	124	L	L	A	T	S	R	F	R	M	N	L	Q	E	E	F	V	C	L	K	S	I	I	L	L	N	S	G	V	T	F	F	X	X	X	X	X	X	X	E	K	D	H	I	R	V	L	D	K	I	T	D	T	L	183				
DB	354	L	L	A	T	V	S	R	F	R	M	L	K	P	E	E	F	V	C	L	K	A	I	L	L	N	S	G	A	F	S	F	-	C	S	N	S	V	E	S	L	H	N	S	S	A	V	E	S	M	L	D	N	I	T	D	A	L	412
QY	184	I	H	L	M	A	K	A	G	L	T	L	Q	Q	H	O	R	L	A	Q	L	L	I	L	S	H	I	R	M	S	N	K	G	M	E	H	L	Y	S	M	K	C	K	N	V	V	P	L	L	L	E	M	L	D	A	243			
DB	413	I	H	H	I	S	H	S	G	A	S	V	Q	Q	P	R	R	Q	V	L	L	L	L	L	S	H	I	R	M	S	N	K	G	M	E	H	L	Y	S	I	K	C	K	N	K	V	P	L	L	L	E	M	L	D	G	472			
QY	244	H	R	L	246																																																						
DB	473	H	R	L	475																																																						

RESULT 10
S71400
estrogen receptor beta - human
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Jun-2000
C:Accession: S71400

R; Mosselman, S.; Polman, J.; Dijkema, R.
 FEBS Lett. 392, 49-53, 1996
 A; Title: ER-beta: identification and characterization of a novel human estrogen receptor
 A; Reference number: S71400; MUID: 96354875; PMID: 8769313
 A; Accession: S71400
 A; Molecule type: mRNA
 A; Residues: 1-477 <MOS>
 A; Cross-references: EMBL: X99101; NID: g1518262; PIDN: CAA67555.1; PID: g1518263
 C; Superfamily: estrogen receptor; erba transforming protein homology
 C; Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone receptor
 F; 94-355/Domain: erba transforming protein homology <ERBA>
 F; 96-116/Region: zinc finger CCCC motif
 F; 132-156/Region: zinc finger CCCC motif
 F; 167-182/Region: nuclear location signal
 F; 52/Binding site: phosphate (Ser) (covalent) (by MAP kinase) #status predicted
 F; 96, 99, 113, 116/Binding site: zinc (Cys) #status predicted
 F; 132, 138, 148, 151/Binding site: zinc (Cys) #status predicted

Query Match	62.2%	Score 764.5;	DB 2;	Length 477;
Best Local Similarity	59.3%	Pred. No. 4.8e-68;		
Matches 144;	Conservative 52;	Mismatches 42;	Indels 5;	Gaps 3;

RESULT 11

JC5939

estrogen receptor beta - human

C;Species: Homo sapiens (man)

C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000

C;Accession: JC5939

R;Ogawa, S.; Inoue, S.; Watanabe, T.; Hiroi, H.; Ozimo, A.; Hosoi, T.; Ouchi, Y.; Muramat

Biochem. Biophys. Res. Commun. 243, 122-126, 1998

A;Title: The complete primary structure of human estrogen receptor beta (hERbeta) and its

A;Reference number: JC5939; MUID:98139878; PMID:9473491

A;Accession: JC5939

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-530 <OGA>

A;Cross-references: DDBJ:AB006590; NID:G2911151; PIDN:BAA24953.1; PID:G2911152

C;Superfamily: estrogen receptor; erba transforming protein homology

F;147-408/Domain: erba transforming protein homology <ERB>

Query Match	62.2%;	Score 764.5;	DB 2;	Length 530;
Best Local Similarity	59.3%;	Pred. No. 5.5e-68;		
Matches 144;	Conservative 52;	Mismatches 42;	Indels 5;	Gaps 3;

Qy 124 LLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKITDTL 183
| | | | | : | | : | | : | | | | : | : | : | | : | : | : | |
Db 380 LLATTSRFRELKLQHKYLCVKAMILLNSSMYPLVTATQADSSRK--LAHLLNAVTDAL 437
| | | | | : | | : | | : | | | | : | : | : | | : | : | : | |
Qy 184 IHLMAKAGLTLOOQHQRLOLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEMLDA 243
: : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 438 VVWIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPLYDLLLEMLNA 497
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 244 HRL 246
| |
Db 498 HVL 500
| |
RESULT 12
A37197
estrogen receptor - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 20-Aug-1999
C;Accession: A37197; A40070
R;Pakdel, F.; Le Gac, F.; Le Goff, P.; Valotaire, Y.
Mol. Endocrinol. 71, 195-204, 1990
A;Title: Full-length sequence and in vitro expression of rainbow trout estrogen receptor
A;Reference number: A37197; MUID:91006824; PMID:2210031
A;Accession: A37197
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-574 <PAK>
A;Cross-references: GB:M31559
R;Pakdel, F.; Le Guellec, C.; Vaillant, C.; Le Roux, M.G.; Valotaire, Y.
Mol. Endocrinol. 3, 44-51, 1989
A;Title: Identification and estrogen induction of two estrogen receptors (ER) messenger
A;Reference number: A40070; MUID:89127284; PMID:2915648
A;Accession: A40070
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 150-574 <PA2>
A;Cross-references: GB:M31559; NID:g213783; PIDN:AAA49552.1; PID:g213784
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zi
F;145-421/Domain: erba transforming protein homology <ERBA>
F;147-167/Region: zinc finger
F;183-207/Region: zinc finger
Query Match 61.7%; Score 758.5; DB 2; Length 574;
Best Local Similarity 62.0%; Pred. No. 2.4e-67;
Matches 147; Conservative 35; Mismatches 54; Indels 1; Gaps 1;
Qy 10 QMVSALLDAEPPILYSEYDPTRPSEASMMGLLTNLADRELVHMINKRVPGFVDITLH 69
: | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 279 EQVLELLQGTALCSRKQVARYTEVTMTLLTSMADKELVHMIWAKKVPGFQELSLH 338
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 70 DQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCKVEGMVEIFDMLLATSS 129
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 339 DQVQLLESSWLEVLMIGLIWRSHCPGKLIFAQDLILDRSEGDCEGMAEIFDMLLATVS 398
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 130 RFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKITDTLIHLMK 189
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 399 RFGMLKLKPEEFVCLKAIILLNPGAFSF-CSNSVESLHNSSAVESMLDNITDALIHISH 457
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 190 AGLTLOOQHQRLOLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEMLDAHRL 246
: | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 458 SGASVQQQPRRQAQLLLLSHIRHMSNKGMEHLYSIKCKNKVPLYDLLLEMLDGHRL 514
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
RESULT 13
JW0046
estrogen receptor beta2 - rat
N;Alternate names: ERbeta2
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 17-Mar-1999
C;Accession: JW0046
R;Maruyama, K.; Endoh, H.; Sasaki-Iwaoaka, H.; Kanou, H.; Shimaya, E.; Hashimoto, S.; Kat
Biochem. Biophys. Res. Commun. 246, 142-147, 1998

A;Title: A novel isoform of rat estrogen receptor beta with 18 amino acid insertion in th
A;Reference number: JW0046; MUID:98262932; PMID:9600083
A;Accession: JW0046
A;Molecule type: mRNA
A;Residues: 1-503 <MAR>
A;Cross-references: DDBJ:AB012721
C;Comment: This protein functions as a negative regulator of estrogen action.
C;Superfamily: estrogen receptor; erba transforming protein homology
F;102-381/Domain: erba transforming protein homology <ERBA>
Query Match 61.0%; Score 750.5; DB 2; Length 503;
Best Local Similarity 55.3%; Pred. No. 1.3e-66;
Matches 146; Conservative 51; Mismatches 44; Indels 23; Gaps 4;
Qy 2 LALSLTADQMVSALLDAEPP-ILYSEYDPTRPSEASMMGLLTNLADRELVHMINKRV 60
| : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 214 LLSTLSPEQLVLTLEAEPPNVLSR--PSMPFTEASMMMSLTKLADKELVHMIGWAKKI 271
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLD----- 107
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 272 PGFVELSLDQVRLLESCWMEVLMVGLMWRSIDHPGKLIFAPDLVDRSSEDPHWHVAQM 331
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 108 -----RNQKCKVEGMVEIFDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTFXXXXX 162
| : | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 332 KSAAPRDEGKCKVEGILEIFDMLLATTSRFRELKLQHKYLCVKAMILLNSSMYPLASANQ 391
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 163 XXXXEEKDHIHRVLDKITDTLIHLMAKAGLTLOOQHQRLOLAQLLLILSHIRHMSNKGMEHL 222
| : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 392 EAESSRK--LTHLLNAVTDALVWVIAKSGISSQQQSVRLANLLMLLSHVRHISNKGMEHL 449
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 223 YSMKCKNVVPLYDLLLEMLDAHRL 246
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 450 LSMKCKNVVPVYDLLLEMLNAHTL 473
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
RESULT 14
S26595
estrogen receptor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S26595
R;Hagen-Mann, K.; Mann, W.; Meyer, H.H.D.
submitted to the EMBL Data Library, May 1992
A;Reference number: S26595
A;Accession: S26595
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-133 <HAG>
A;Cross-references: UNIPROT:P49884; EMBL:X66841; NID:g334; PIDN:CAA47317.1; PID:g335
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: steroid hormone receptor; zinc finger
F;1-87/Domain: erba transforming protein homology (fragment) <ERBA>
Query Match 50.9%; Score 626.5; DB 2; Length 133;
Best Local Similarity 92.5%; Pred. No. 5.4e-55;
Matches 124; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
Qy 66 LTLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCKVEGMVEIFDMLL 125
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 1 LTLHDQVHLLCAWLEILMIGLVWRSMEHPVKLLFAPNLLDRNQKCKVEGMVEIFDMLL 60
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 126 ATSSRFRMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKITDTLIH 185
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 61 ATSSRFRMMNLQGEFVCLKSIILLNSGVYTF-LSTLKSLEEKDHIHRVLDKITDTLIH 119
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 186 LMAKAGLTLOQQHQ 199
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 120 LMAKAGLTLOQQHQ 133
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
RESULT 15
I67419
estradiol receptor - rhesus macaque (fragment)

C;Species: Macaca mulatta (rhesus macaque)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C;Accession: I67419
R;Chandrasekhar, Y.A.; Melner, M.H.; Nagalla, S.R.; Stouffer, R.L.
Endocrinology 135, 307-314, 1994
A;Title: Progesterone receptor, but not estradiol receptor, messenger ribonucleic acid
A;Reference number: I53287; MUID:94283272; PMID:8013365
A;Accession: I67419
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-121 <RES>
A;Cross-references: UNIPROT:P49886; GB:S71040; NID:g547182; PIDN:AAB31102.1; PID:g547183
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: steroid hormone receptor; zinc finger
F;1-54/Domain: erba transforming protein homology (fragment) <ERBA>

Query Match 44.5%; Score 547.5; DB 2; Length 121;
Best Local Similarity 91.0%; Pred. No. 3.5e-47;
Matches 111; Conservative 1; Mismatches 9; Indels 1; Gaps 1;
Qy 99 LFAPNLLLDNRNQKCVEGMVEIFDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTFX 158
|||
Db 1 LFAPNLLLDNRNQKCVEGMVEISFDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF- 59
Qy 159 XXXXXXXXEEKDHIHRVLDKITDTLIHLMKAGLTQQQHQRLAQLLLILSHIRHMSNKG 218
|||
Db 60 LSSTLKSLEEKDHIHRVLDKITDTLIHLMKAGLTQQQHRRLAQLLLILSHIRHMSNKG 119
Qy 219 ME 220
||
Db 120 ME 121

Search completed: November 8, 2004, 08:28:28
Job time : 12.049 secs

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Qy	61	PGFVDTLTHDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVEGMVEI	120
Db	182	PGFVDTLTHDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVEGMVEI	241
Qy	121	FDMLLATSSRFRMMNLQGEFVCLSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT	180
Db	242	FDMLLATSSRFRMMNLQGEFVCLSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT	300
Qy	181	DTLIHLMKAGLTLOQOQHORLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM	240
Db	301	DTLIHLMKAGLTLOQOQHORLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM	360
Qy	241	LDAHRL	246
Db	361	LDAHRL	366

```

RESULT 2
US-157-899A-4
; Sequence 4, Application US/10157899A
; Publication No. US20030143559A1
; GENERAL INFORMATION:
; APPLICANT: Bracken, Kathryn Rene
; APPLICANT: de los Angeles, Joseph Ernest
; APPLICANT: Huang, Ying
; APPLICANT: Kadan, Michael Joseph
; APPLICANT: Ksander, Gary Michael
; APPLICANT: Zerby, Dennis
; TITLE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL
; TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 4-32018A
; CURRENT APPLICATION NUMBER: US/10/157,899A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/294,839
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion of the human-Estrogen-receptor-ligand-binding-domain and
; OTHER INFORMATION: zinc finger array(C7)
US-10-157-899A-4

```

Query Match	98.1%	Score 1206.5;	DB 14;	Length 438;
Local Similarity	96.3%	Pred. No. 2.4e-125;		
Mismatches 237;	Conservative 0;	Mismatches 8;	Indels 1;	Gaps 1;
Qy 1	SLALSLTADQMVSA	LLDAEPPILYSEYD	TRPFSEASMMGL	LTNLADRELVHMINWAKRV 60
Db 146	SLALSLTADQMVSA	LLDAEPPILYSEYD	TRPFSEASMMGL	LTNLADRELVHMINWAKRV 205
Qy 61	PGFVDLTLDQVHLL	ECAWLEILMIGLV	WRSMHPGKLLFAP	NLLDRNQKCVEGMVEI 120
Db 206	PGFVDLTLDQVHLL	ECAWLEILMIGLV	WRSMHPGKLLFAP	NLLDRNQKCVEGMVEI 265
Qy 121	FDMLLATSSRFRMN	LQGEFVCLKSIIL	NSGVYTFXXXXXX	XXXXXEEKDHIHRVLDKIT 180
Db 266	FDMLLATSSRFRMN	LQGEFVCLKSIIL	NSGVYTF-LSSTL	KSLEEKDHIHRVLDKIT 324
Qy 181	DTLIHLMAKAGLT	LQQQHQRLAQLL	ILSHIRHMSNKGME	HLYSMKCKNVVPLYDLLLEM 240
Db 325	DTLIHLMAKAGLT	LQQQHQRLAQLL	ILSHIRHMSNKGME	HLYSMKCKNVVPLYDLLLEM 384
Qy 241	LDAHRL	246		
Db 385	LDAHRL	390		

RESULT 3

```

US-09-853-033-2
; Sequence 2, Application US/09853033
; Patent No. US20020100068A1
; GENERAL INFORMATION:
; APPLICANT: CHAMBON, PIERRE
; APPLICANT: METZGER, DANIEL
; TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
; TITLE OF INVENTION: MEDIATED BY MODIFIED CRE-ER
; FILE REFERENCE: 065691/0222
; CURRENT APPLICATION NUMBER: US/09/853,033
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: FR 00/12570
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-033-2

```

Query Match	98.1%	Score 1206.5;	DB 9;	Length 595;			
Best Local Similarity	96.3%	Pred. No. 3.5e-125;					
Matches 237; Conservative	0;	Mismatches 8;	Indels 1;	Gaps 1			
QY	1	SLALSLTADQMVSA	LDAPPILYSEYDPT	TRPFSEASMMGLLTNLADREL	VHMINWAKRV	60	
DB	305	SLALSLTADQMVSA	LDAPPILYSEYDPT	TRPFSEASMMGLLTNLADREL	VHMINWAKRV	364	
QY	61	PGFVDLT	TLHDQVHLL	ECAWLEILMIGLV	WRSMHPGKLIFAPNLLDRNQK	CGVEGMVEI	120
DB	365	PGFVDLT	TLHDQVHLL	ECAWLEILMIGLV	WRSMHPGKLIFAPNLLDRNQK	CGVEGMVEI	424
QY	121	FDMLLATSSRFR	MNMQGEHFVCL	KSIILLNSGVYTF	FXXXXXXXXXXXE	KDHIHRVLDKIT	180
DB	425	FDMLLATSSRFR	MNMQGEHFVCL	KSIILLNSGVYTF	LSSTLKSLEEKD	HIHRVLDKIT	483
QY	181	DTLIHLM	AKAGTLQQQHQR	LAQLLLILSHIRH	MSNKGMEHLYSMKCKNVV	PLYDLLLEM	240
DB	484	DTLIHLM	AKAGTLQQQHQR	LAQLLLILSHIRH	MSNKGMEHLYSMKCKNVV	PLYDLLLEM	543
QY	241	LDAHRL	246				
DB	544	LDAHRL	549				

RESULT 4
US-10-148-835-1
; Sequence 1, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 595
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-148-835-1

	Query Match	98.1%;	Score 1206.5;	DB 14;	Length 595;
	Best Local Similarity	96.3%;	Pred. No. 3.5e-125;		
	Matches 237;	Conservative	0;	Mismatches 8;	Indels 1; Gaps 1
QY	1	SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV	60		
Db	305	SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV	364		
QY	61	PGFVDLTLDHQVHLLLECAWLEILMIGLVWRSMHPGKLLFAPNLLLDNRNQKCKVEGMVEI	120		

Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 424
QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db 425 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483
QY 181 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLLEM 240
Db 484 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLLEM 543
QY 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 5
US-10-148-835-2
; Sequence 2, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-2

Query Match 98.1%; Score 1206.5; DB 14; Length 595;
Best Local Similarity 96.3%; Pred. No. 3.5e-125;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120
Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 424
QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db 425 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483
QY 181 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLLEM 240
Db 484 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLLEM 543
QY 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 6
US-10-148-835-9
; Sequence 9, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 595

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-9
Query Match 98.1%; Score 1206.5; DB 14; Length 595;
Best Local Similarity 96.3%; Pred. No. 3.5e-125;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120
Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 424
QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db 425 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483
QY 181 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLLEM 240
Db 484 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLLEM 543
QY 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 7
US-10-148-835-5
; Sequence 5, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-5

Query Match 97.8%; Score 1202.5; DB 14; Length 595;
Best Local Similarity 95.9%; Pred. No. 9.9e-125;
Matches 236; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120
Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 424
QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db 425 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483
QY 181 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLLEM 240
Db 484 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLLEM 543
QY 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 8

US-10-148-835-3
; Sequence 3, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-3

Query Match 97.6%; Score 1200.5; DB 14; Length 595;
Best Local Similarity 95.9%; Pred. No. 1.7e-124;
Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALFLTADQMVSAALLDAEPPILYSEYDPTRPFSSEASMMGLLTNLADRELVHMINWAKRV 364

Qy 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVGMEI 120
Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVGMEI 424

Qy 121 FDMLLATSSRFRMMNLQGEFEFVCLKSIILLNSGVYTFXXXXXXXEEKDHHRVLDKIT 180
Db 425 FDMLLATSSRFRMMNLQGEFEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHHRVLDKIT 483

Qy 181 DTLIHLMAKAGLTLOQQHORLAQLLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEEM 240
Db 484 DTLIHLMAKAGLTLOQQHORLAQLLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEEM 543

Qy 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 9
US-10-148-835-4
; Sequence 4, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-4

Query Match 97.5%; Score 1199.5; DB 14; Length 595;
Best Local Similarity 95.9%; Pred. No. 2.1e-124;
Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSSEASMMGLLTNLADRELVHMINWAKRV 364

Qy 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVGMEI 120
Db 365 PGFVDLTLDQVHLLLECAWLEILMIDLVWRSMEHPGKLLFAPNLLLDNRNQKCVGMEI 424

Qy 121 FDMLLATSSRFRMMNLQGEFEFVCLKSIILLNSGVYTFXXXXXXXEEKDHHRVLDKIT 180

Db 425 FDMLLATSSRFRMMNLQGEFEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHHRVLDKIT 483

Qy 181 DTLIHLMAKAGLTLOQQHORLAQLLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEEM 240
Db 484 DTLIHLMAKAGLTLOQQHORLAQLLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEEM 543

Qy 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 10
US-10-148-835-10
; Sequence 10, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-10

Query Match 97.5%; Score 1199.5; DB 14; Length 595;
Best Local Similarity 95.9%; Pred. No. 2.1e-124;
Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSSEASMMGLLTNLADRELVHMINWAKRV 364

Qy 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVGMEI 120
Db 365 PGFVDLTLDQVHLLLECAWLEILMIDLVWRSMEHPGKLLFAPNLLLDNRNQKCVGMEI 424

Qy 121 FDMLLATSSRFRMMNLQGEFEFVCLKSIILLNSGVYTFXXXXXXXEEKDHHRVLDKIT 180
Db 425 FDMLLATSSRFRMMNLQGEFEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHHRVLDKIT 483

Qy 181 DTLIHLMAKAGLTLOQQHORLAQLLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEEM 240
Db 484 DTLIHLMAKAGLTLOQQHORLAQLLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEEM 543

Qy 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 11
US-10-148-835-8
; Sequence 8, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-8

Query Match	97.4%;	Score 1198.5;	DB 14;	Length 595;
Best Local Similarity	95.5%;	Pred. No. 2.8e-124;		
Matches 235;	Conservative 2;	Mismatches 8;	Indels 1;	Gaps 1;
QY 1	SLALSLTADQMV	SALLDAEPPILYSEYDPT	TRPFSEASMMGILLTNLADREL	VHMINWAKRV 60
Db				
305	SLALSLTADQMV	SALLDAEPPILYSEYDPT	TRPFSEASMMGILLTNLADREL	VHMINWAKRV 364
QY 61	PGFVDLTLDQV	HLLECAWLEILMIGLV	WRSMHPGKLLFAPNLL	LLDRNOGKCV
Db				
365	PGFVDLTLDQV	HLLECAWLEILMIGLV	WRSMHPGKLLFAPNLL	LLDRNOGKCV
QY 121	FDMLLATSSR	FRMMNLQGEHFVCLKSI	ILLNSGVYTFXXXXXX	XXXXXKDHHRVLDKIT 180
Db				
425	FDMLLATSSR	FRMMNLQGEHFVCLKSI	ILLNSGVYTF-LSSTLKS	LEEKDHIHRVLDKIT 483
QY 181	DTLIHLMKAGL	TLOOQHQR	LAQLLLILSHIRHMS	NKGMHLYSMKCQNVVPL
Db				
484	DTLIHLMKAGL	TLOOQHQR	LAQLLLILSHIRHMS	NKGMHLYSMKCQNVVPL
QY 241	LDAHRL	246		
Db				
544	LDAHRL	549		

RESULT 12
US-09-853-033-4
; Sequence 4, Application US/09853033
; Patent No. US20020100068A1
; GENERAL INFORMATION:
; APPLICANT: CHAMBON, PIERRE
; APPLICANT: METZGER, DANIEL
; TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
; TITLE OF INVENTION: MEDIATED BY MODIFIED CRE-ER
; FILE REFERENCE: 065691/0222
; CURRENT APPLICATION NUMBER: US/09/853, 033
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: FR 00/12570
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 4
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric sequence
; OTHER INFORMATION: Homosapiens-Bacteriophage P1
US-09-853-033-4

Query Match	97.4%	Score 1198.5;	DB 9;	Length 660;
Best Local Similarity	95.9%	Pred. No. 3.2e-124;		
Matches 236;	Conservative	0;	Mismatches 9;	Indels 1;
Gaps	1;			
Qy	1	SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINKRV	60	
Db	370	SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINKRV	429	
Qy	61	PGFVDLTLDQVHLLCEAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEI	120	
Db	430	PGFVDLTLDQVHLLCEAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEI	489	
Qy	121	FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT	180	
Db	490	FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSSTLKSLEEKDHIHRVLDKIT	548	
Qy	181	DTLIHLMKAGLTLOQOQHORLAQLLLLSHIRHMSNKGMEHLYSMCKKNVPLYDLLLLM	240	
Db	549	DTLIHLMKAGLTLOQOQHORLAQLLLLSHIRHMSNKRMEHLYSMCKKNVPLYDLLLLM	608	
Qy	241	LDAHRL	246	
Db	609	LDAHRL	614	

RESULT 13
US-10-157-899A-8
; Sequence 8, Application US/10157899A
; Publication No. US20030143559A1
; GENERAL INFORMATION:
; APPLICANT: Bracken, Kathryn Rene
; APPLICANT: de los Angeles, Joseph Ernest
; APPLICANT: Huang, Ying
; APPLICANT: Kadan, Michael Joseph
; APPLICANT: Ksander, Gary Michael
; APPLICANT: Zerby, Dennis
; TITLE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL
; TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 4-32018A
; CURRENT APPLICATION NUMBER: US/10/157,899A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/294,839
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion of a mutated human-Estrogen-receptor-ligand-binding-domain
; OTHER INFORMATION: and a zinc finger array (C7)
US-10-157-899A-8

Query Match	97.4%	Score 1197.5;	DB 14;	Length 414;
Best Local Similarity	95.5%	Pred. No. 2.2e-124;		
Matches 235;	Conservative	1;	Mismatches 9;	Indels 1;
QY	1	SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV	60	
Db	122	SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV	181	
QY	61	PGFVDLTLDQVHLLHLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCKVEGMVEI	120	
Db	182	PGFVDLTLDQVHLLHLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCKVEGMVEI	241	
QY	121	FDMLLATSSRFMRMNVLQGEFVCLKSIILLNSGVYTFXXXXXXXKDHHRVLDKIT	180	
Db	242	FDMLATSSRFMRMNVLQGEFVCLKSIILLNSGVYTF-LSSSTLKSLEEKDHIHRVLDKIT	300	
QY	181	DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKCNVPLYDLLEEM	240	
Db	301	DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKCNVPLYDLLEEM	360	
QY	241	LDAHRL	246	
Db	361	LDAHRL	366	

RESULT 14

US-10-157-899A-14

; Sequence 14, Application US/10157899A

; Publication No. US20030143559A1

; GENERAL INFORMATION:

; APPLICANT: Bracken, Kathryn Rene

; APPLICANT: de los Angeles, Joseph Ernest

; APPLICANT: Huang, Ying

; APPLICANT: Kadan, Michael Joseph

; APPLICANT: Ksander, Gary Michael

; APPLICANT: Zerby, Dennis

; TITLE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS A

; TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS

; FILE REFERENCE: 4-32018A

; CURRENT APPLICATION NUMBER: US/10/157,899A

; CURRENT FILING DATE: 2002-09-12

; PRIOR APPLICATION NUMBER: US 60/294,839

; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion of a mutated human-Estrogen-receptor-ligand-binding-domain
; OTHER INFORMATION: and a zinc finger array(C7)
US-10-157-899A-14

Query Match 97.4%; Score 1197.5; DB 14; Length 438;
Best Local Similarity 95.5%; Pred. No. 2.4e-124;
Matches 235; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db |||||
SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 205

QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVGMEVEI 120
Db |||||
PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVGMEVEI 265

QY 121 FDMLLATSSRFRMMNLQGEFEVCLKSIILLNSGVYTFXXXXXXXEKKDHIHRVLDKIT 180
Db |||||
FDMALATSSRFRMMNLQGEFEVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 324

QY 181 DTLIHLMAKAGLTQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVPLYDLLEEM 240
Db |||||
DTLIHLMAKAGLTQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVPLYDLLEEM 384

QY 241 LDAHRL 246
Db |||||
385 LDAHRL 390

RESULT 15
US-10-006-760-19
; Sequence 19, Application US/10006760
; Publication No. US20030186385A1
; GENERAL INFORMATION:
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND
; TITLE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF
; FILE REFERENCE: 176/60901
; CURRENT APPLICATION NUMBER: US/10/006,760
; OR FILING DATE: 2001-11-19
; OR APPLICATION NUMBER: 60/249,756
; OR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: lexA-ER(alpha)EF fusion protein
US-10-006-760-19

Query Match 97.4%; Score 1197.5; DB 14; Length 511;
Best Local Similarity 95.9%; Pred. No. 2.9e-124;
Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db |||||
SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 280

QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVGMEVEI 120
Db |||||
PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPVKKLLFAPNLLLDNRNQKCVGMEVEI 340

QY 121 FDMLLATSSRFRMMNLQGEFEVCLKSIILLNSGVYTFXXXXXXXEKKDHIHRVLDKIT 180
Db |||||
341 FDMLLATSSRFRMMNLQGEFEVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 399

QY 181 DTLIHLMAKAGLTQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVPLYDLLEEM 240
Db |||||
400 DTLIHLMAKAGLTQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVPLYDLLEEM 459

QY 241 LDAHRL 246
Db |||||
460 LDAHRL 465

Search completed: November 8, 2004, 08:42:50
Job time : 38.151 secs

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OM protein - protein search, using sw model

Run on: November 8, 2004, 08:16:47 ; Search time 14.5592 Seconds
(without alignments)
1120.546 Million cell updates/sec

Title: US-09-830-693B-28
Perfect score: 1230
Sequence: 1 SLALSLTADQMVSALLDAEP.....CKNVVPLYDLLLEMLDAHRL 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1206.5	98.1	595	3	US-08-764-870-12 Sequence 12, Appl
2	1206.5	98.1	595	3	US-08-980-115-12 Sequence 12, Appl
3	1197.5	97.4	591	2	US-08-836-620A-17 Sequence 17, Appl
4	1197.5	97.4	595	3	US-09-041-886-35 Sequence 35, Appl
5	1197.5	97.4	595	4	US-08-453-998-2 Sequence 2, Appl
6	1197.5	97.4	651	3	US-08-693-940-3 Sequence 3, Appl
7	1197.5	97.4	651	4	US-09-566-660-3 Sequence 3, Appl
8	1197.5	97.4	773	3	US-08-564-264-1 Sequence 1, Appl
9	1180	95.9	410	6	5223606-5 Patent No. 5223606
10	1167.5	94.9	596	2	US-08-836-620A-16 Sequence 16, Appl
11	1146	93.2	264	4	US-09-660-979-1 Sequence 1, Appl
12	961.5	78.2	243	2	US-08-836-620A-10 Sequence 10, Appl
13	951.5	77.4	243	2	US-08-836-620A-9 Sequence 9, Appl
14	946.5	77.0	243	2	US-08-836-620A-8 Sequence 8, Appl
15	792.5	64.4	575	4	US-09-893-666A-2 Sequence 2, Appl
16	769.5	62.6	484	2	US-08-836-620A-13 Sequence 13, Appl
17	769.5	62.6	485	2	US-08-836-620A-2 Sequence 2, Appl
18	764.5	62.2	477	4	US-09-608-088-5 Sequence 5, Appl
19	764.5	62.2	477	4	US-09-711-288-5 Sequence 5, Appl
20	764.5	62.2	485	2	US-08-836-620A-3 Sequence 3, Appl
21	764.5	62.2	530	4	US-09-608-088-25 Sequence 25, Appl
22	764.5	62.2	530	4	US-09-711-288-25 Sequence 25, Appl
23	764.5	62.2	548	3	US-09-139-617-1 Sequence 1, Appl
24	764.5	62.2	548	4	US-09-561-741A-1 Sequence 1, Appl
25	764.5	62.2	548	4	US-09-558-795-1 Sequence 1, Appl
26	757.5	61.6	484	2	US-08-836-620A-14 Sequence 14, Appl
27	757.5	61.6	485	2	US-08-836-620A-5 Sequence 5, Appl

28	752.5	61.2	233	4	US-09-608-088-4 Sequence 4, Appli
29	752.5	61.2	233	4	US-09-711-288-4 Sequence 4, Appli
30	730	59.3	229	3	US-09-249-645-1 Sequence 1, Appli
31	726	59.0	229	4	US-09-844-132B-1 Sequence 1, Appli
32	700.5	57.0	228	3	US-09-249-645-2 Sequence 2, Appli
33	700.5	57.0	228	4	US-09-844-132B-2 Sequence 2, Appli
34	667	54.2	226	2	US-08-836-620A-7 Sequence 7, Appli
35	623.5	50.7	384	2	US-08-836-620A-15 Sequence 15, Appl
36	623.5	50.7	416	4	US-09-608-088-6 Sequence 6, Appli
37	623.5	50.7	416	4	US-09-711-288-6 Sequence 6, Appli
38	623.5	50.7	418	4	US-09-608-088-21 Sequence 21, Appl
39	623.5	50.7	418	4	US-09-711-288-21 Sequence 21, Appl
40	514	41.8	97	4	US-09-652-345-5 Sequence 5, Appli
41	385.5	31.3	435	3	US-09-040-508-2 Sequence 2, Appli
42	385.5	31.3	435	3	US-09-500-654-2 Sequence 2, Appli
43	385.5	31.3	458	3	US-09-141-000-4 Sequence 4, Appli
44	376.5	30.6	431	2	US-08-836-620A-19 Sequence 19, Appl
45	375.5	30.5	500	3	US-09-141-000-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-764-870-12
; Sequence 12, Application US/08764870
; Patent No. 6236946
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Thomas S
; APPLICANT: Baxter, John D
; APPLICANT: Fletcher, Robert J
; APPLICANT: Wagner, Richard L
; APPLICANT: Kushner, Peter J
; APPLICANT: Apriletti, James W
; APPLICANT: West, Brian
; TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand
; TITLE OF INVENTION: Binding Domains
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,870
; FILING DATE: 13-DEC-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/008,540
; FILING DATE: 13-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/008,543
; FILING DATE: 13-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/008,606
; FILING DATE: 14-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N
; REGISTRATION/DOCKET NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: UCAL-246/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)843-5000
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 595 amino acids
; TYPE: amino acid

QY 181 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLL 240
Db 484 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLL 543
QY 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 4
US-09-041-886-35
; Sequence 35, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 595 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-041-886-35

Query Match 97.4%; Score 1197.5; DB 3; Length 595;
Best Local Similarity 95.9%; Pred. No. 3.6e-133;
Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMVEI 120
Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMVEI 424
QY 121 FDMLLATSSRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHHRVLDKIT 180
Db 425 FDMLLATSSRFRMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHHRVLDKIT 483
QY 181 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLL 240
Db 484 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLL 543
QY 241 LDAHRL 246
|||||

Db 544 LDAHRL 549
RESULT 5
US-08-453-998-2
; Sequence 2, Application US/08453998
; Patent No. 6444438
; GENERAL INFORMATION:
; APPLICANT: CHAMBER, PIERRE
; APPLICANT: METZGER, DANIEL
; APPLICANT: WHITE, JOHN
; TITLE OF INVENTION: METHOD FOR THE PREPARATION OF A PROTEIN
; TITLE OF INVENTION: BY YEASTS USING AN INDUCIBLE SYSTEM, VECTORS AND
; TITLE OF INVENTION: CORRESPONDING TRANSFORMED STRAINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVE., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,998
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/161,064
; FILING DATE: 03-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAPIN, MARLANA K.
; REGISTRATION NUMBER: 35,843
; REFERENCE/DOCKET NUMBER: 1037/98493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 595 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-453-998-2

Query Match 97.4%; Score 1197.5; DB 4; Length 595;
Best Local Similarity 95.9%; Pred. No. 3.6e-133;
Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFPSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMVEI 120
Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMVEI 424
QY 121 FDMLLATSSRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHHRVLDKIT 180
Db 425 FDMLLATSSRFRMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHHRVLDKIT 483
QY 181 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLL 240
Db 484 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLL 543
QY 241 LDAHRL 246
|||||

Db 544 LDAHRL 549

RESULT 6

US-08-693-940-3

; Sequence 3, Application US/08693940

; Patent No. 6133027

; GENERAL INFORMATION:

; APPLICANT: Yee, Jiing-Kuan

; APPLICANT: Friedman, Theodore

; APPLICANT: Chen, Shin-Tai

; TITLE OF INVENTION: Inducible Expression System

; TITLE OF INVENTION: Useful in the Generation of Packaging Cell Lines for

; TITLE OF INVENTION: Pseudotyped Retroviral Vectors

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bozicevic & Reed, LLP

; STREET: 285 Hamilton Ave, Suite 200

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/693,940

; FILING DATE: 07-AUG-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Francis, Carol L

; REGISTRATION NUMBER: 36,513

; REFERENCE/DOCKET NUMBER: 6510-055001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-327-3400

; TELEFAX: 650-327-3231

; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 651 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

US-08-693-940-3

Query Match 97.4%; Score 1197.5; DB 3; Length 651;

Best Local Similarity 95.9%; Pred. No. 4.1e-133;

Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 60

Db 361 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 420

QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPVKLLFAPNLLLDNRNQGKCVGMEVEI 120

Db 421 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPVKLLFAPNLLLDNRNQGKCVGMEVEI 480

QY 121 FDMLLATSSRFRMMNLQGEFEVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180

Db 481 FDMLLATSSRFRMMNLQGEFEVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 539

QY 181 DTLIHLMKAGLTLQQQHQRLAQLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEM 240

Db 540 DTLIHLMKAGLTLQQQHQRLAQLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEM 599

QY 241 LDAHRL 246

Db 600 LDAHRL 605

RESULT 7

US-09-566-660-3

; Sequence 3, Application US/095666660

; Patent No. 6432705

; GENERAL INFORMATION:

; APPLICANT: Yee, Jiing-Kuan

; APPLICANT: Friedman, Theodore

; APPLICANT: Chen, Shin-Tai

; TITLE OF INVENTION: Inducible Expression System

; FILE REFERENCE: 6510-055CON

; CURRENT APPLICATION NUMBER: US/09/566,660

; CURRENT FILING DATE: 2000-05-08

; PRIOR APPLICATION NUMBER: 08/693,940

; PRIOR FILING DATE: 1996-08-07

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 651

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Multi-chimeric transactivating factor

US-09-566-660-3

Query Match 97.4%; Score 1197.5; DB 4; Length 651;

Best Local Similarity 95.9%; Pred. No. 4.1e-133;

Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 60

Db 361 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 420

QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPVKLLFAPNLLLDNRNQGKCVGMEVEI 120

Db 421 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPVKLLFAPNLLLDNRNQGKCVGMEVEI 480

QY 121 FDMLLATSSRFRMMNLQGEFEVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180

Db 481 FDMLLATSSRFRMMNLQGEFEVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 539

QY 181 DTLIHLMKAGLTLQQQHQRLAQLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEM 240

Db 540 DTLIHLMKAGLTLQQQHQRLAQLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEM 599

QY 241 LDAHRL 246

Db 600 LDAHRL 605

RESULT 8

US-08-564-264-1

; Sequence 1, Application US/08564264

; Patent No. 6040430

; GENERAL INFORMATION:

; APPLICANT: STEWART, Francis

; TITLE OF INVENTION: REGULATION OF SITE-SPECIFIC

; TITLE OF INVENTION: RECOMBINATION BY SITE-SPECIFIC RECOMBINASE/NUCLEAR

; TITLE OF INVENTION: RECEPTOR FUSION PROTEINS

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram

; STREET: 655 Fifteenth Street N.W. Suite 330

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005-5701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

Db 600 LDAHRL 605

RESULT 7

US-09-566-660-3

; Sequence 3, Application US/095666660

; Patent No. 6432705

; GENERAL INFORMATION:

; APPLICANT: Yee, Jiing-Kuan

; APPLICANT: Friedman, Theodore

; APPLICANT: Chen, Shin-Tai

; TITLE OF INVENTION: Inducible Expression System

; FILE REFERENCE: 6510-055CON

; CURRENT APPLICATION NUMBER: US/09/566,660

; CURRENT FILING DATE: 2000-05-08

; PRIOR APPLICATION NUMBER: 08/693,940

; PRIOR FILING DATE: 1996-08-07

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 651

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Multi-chimeric transactivating factor

US-09-566-660-3

Query Match 97.4%; Score 1197.5; DB 4; Length 651;

Best Local Similarity 95.9%; Pred. No. 4.1e-133;

Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 60

Db 361 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 420

QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPVKLLFAPNLLLDNRNQGKCVGMEVEI 120

Db 421 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPVKLLFAPNLLLDNRNQGKCVGMEVEI 480

QY 121 FDMLLATSSRFRMMNLQGEFEVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180

Db 481 FDMLLATSSRFRMMNLQGEFEVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 539

QY 181 DTLIHLMKAGLTLQQQHQRLAQLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEM 240

Db 540 DTLIHLMKAGLTLQQQHQRLAQLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEM 599

QY 241 LDAHRL 246

Db 600 LDAHRL 605

RESULT 8

US-08-564-264-1

; Sequence 1, Application US/08564264

; Patent No. 6040430

; GENERAL INFORMATION:

; APPLICANT: STEWART, Francis

; TITLE OF INVENTION: REGULATION OF SITE-SPECIFIC

; TITLE OF INVENTION: RECOMBINATION BY SITE-SPECIFIC RECOMBINASE/NUCLEAR

; TITLE OF INVENTION: RECEPTOR FUSION PROTEINS

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram

; STREET: 655 Fifteenth Street N.W. Suite 330

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005-5701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,264
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02088
FILING DATE: 28-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 110 298.2
FILING DATE: 28-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Murray, Robert B.
REGISTRATION NUMBER: 22,980
REFERENCE/DOCKET NUMBER: P564-5019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 773 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc feature
LOCATION: (1-423)
OTHER INFORMATION: /note= "FLP recombinase domain."
FEATURE:
NAME/KEY: misc feature
LOCATION: (424-428)
OTHER INFORMATION: /note= "Linker peptide."
FEATURE:
NAME/KEY: misc feature
LOCATION: (429-773)
OTHER INFORMATION: /note= "Estrogen binding domain."
US-08-564-264-1

Query Match 97.4%; Score 1197.5; DB 3; Length 773;
Best Local Similarity 95.9%; Pred. No. 5.2e-133;
Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTFPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 483 SLALSLTADQMVSAALLDAEPPILYSEYDPTFPFSEASMMGLLTNLADRELVHMINWAKRV 542
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120
Db 543 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 602
QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHHRVLDKIT 180
Db 603 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHHRVLDKIT 661
QY 181 DTLIHLMKAGLTLOQOQHORLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLL 240
Db 662 DTLIHLMKAGLTLOQOQHORLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLL 721
QY 241 LDAHRL 246
Db 722 LDAHRL 727

RESULT 9
5223606-5
Patent No. 5223606
APPLICANT: BLAUDIN DE THE, HUGHES;MARCHIO, AGNES;TIOILLAIS,
PIERRE;DEJEAN, ANNE
TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED
PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/134,130
FILING DATE: 17-DEC-1987
PRIOR APPLICATION DATA:
SEQ ID NO:5:
LENGTH: 410
5223606-5
Query Match 95.9%; Score 1180; DB 6; Length 410;
Best Local Similarity 95.5%; Pred. No. 2.5e-131;
Matches 235; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTFPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 121 SLALSLTADQMVSAALLDAE-PILYSEYDPTFPFSEASMMGLLTNLADRELVHMINWAKRV 179
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120
Db 180 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPVKKLLFAPNLLDRNQKCVGMEI 239
QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHHRVLDKIT 180
Db 240 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHHRVLDKIT 298
QY 181 DTLIHLMKAGLTLOQOQHORLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLL 240
Db 299 DTLIHLMKAGLTLOQOQHORLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLL 358
QY 241 LDAHRL 246
Db 359 LDAHRL 364

RESULT 10
US-08-836-620A-16
Sequence 16, Application US/08836620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Rattus rattus
US-08-836-620A-16
Query Match 94.9%; Score 1167.5; DB 2; Length 596;
Best Local Similarity 92.7%; Pred. No. 1.3e-129;

	Matches	228;	Conservative	5;	Mismatches	12;	Indels	1;	Gaps	1;
QY	1	SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADELVHMINWAKRV	60							
Dd	310	SPALSLTADQMVSALLDAEPPILYSEYDPSRPFSEASMMGLLTNLADELVHMINWAKRV	369							
QY	61	PGFVDLTLHDQVHLLECAWLLEIMIGLVWRSMHPGKLLFAPNLILLDRNQKCVEGMVEI	120							
Dd	370	PGFGDLNLHDQVHLLECAWLLEIMIGLVWRSMHPGKLLFAPNLILLDRNQKCVEGMVEI	429							
QY	121	FDMLLATSSRRFRMNNLQGEHFVCLKSIIILNSGVYTFXXXXXXXEEKDHHRVLDKIT	180							
Dd	430	FDMLLATSSRRFRMNNLQGEHFVCLKSIIILNSGVYTF-LSSTLKSLEEKDHHRVLDKIN	488							
QY	181	DTLIHLMKAAGLTLOQQHORLAQLLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM	240							
Dd	489	DTLIHLMKAAGLTLOQQHRRLAQLLLLILSHIRHMSNKGMEHLYNMCKKNVVPLYDLLLEM	548							
QY	241	LDAHRL	246							
Dd	549	LDAHRL	554							

RESULT 11
US-09-660-979-1
; Sequence 1, Application US/09660979
; Patent No. 6500629
; GENERAL INFORMATION:
; APPLICANT: Cleaver, Brian
; APPLICANT: Green, Mike L.
; TITLE OF INVENTION: Materials and Methods for Detection and Quantitation of an Analyte
; FILE REFERENCE: ELI-101XCL
; CURRENT APPLICATION NUMBER: US/09/660,979
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,627
; PRIOR FILING DATE: 1999-09-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Equus
US-09-660-979-1

Query Match	93.2%;	Score 1146;	DB 4;	Length 264;		
Best Local Similarity	91.5%;	Pred. No. 1.4e-127;				
Matches 225;	Conservative	7;	Mismatches 12;	Indels 2;		
Gaps	2;					
QY	1	SLALSLTADQMVSA	LLDAEPPILYSEYDPT	TRPFSEASMGLLTNLADREL	VHMINWAKRV	60
DB	5	SPVLSLTAEQMIS	ALLDAEPPVLYSEYDAT	TRPFNEASMGLLTNLADREL	VHMINWAKRV	64
QY	61	PGFVDLTLHDQV	HLLECAWLEILMIGLV	WRSMHPGKLLFAPNLL	LDNRQK	120
DB	65	PGFVDLSLHDQV	HLLECAWLEILMIGLV	WRSMHPGKLLFAPNLL	LDNRQK	124
QY	121	FDMLLATSSRFR	MNMLQGEFVCLKSI	ILLNSGVYTFXXXXXX	XXXXXKDH	180
DB	125	FDMLLATSSRLR	MNMLQGEFVCLKSI	ILLNSGVYTF-L	SSSTLKSLEEKD	183
QY	181	DTLIHLMKAGLT	TQQQHQRLAQ	LLLLILSHIRMSNKG	MEHLYSMCKCN	240
DB	184	DTLIHLMKAGLT	-QQHRRLAQ	LLLLILSHIRMSNKG	MEHLYSMCKCN	242
QY	241	LDAHRL				
DB	243	LDAHRL				

RESULT 12
US-08-836-620A-10
; Sequence 10, Application US/08836620A
; Patent No.5958710

```

;
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Orphan receptor
; NUMBER OF SEQUENCES: 19
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,620A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/03933
; FILING DATE:
; APPLICATION NUMBER: GB 9518272.1
; FILING DATE: 08-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9605550.4
; FILING DATE: 15-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9607532.0
; FILING DATE: 11-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9609576.5
; FILING DATE: 08-MAY-1996
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
US-08-836-620A-10

Query Match 78.2%; Score 961.5; DB 2; Length
Best Local Similarity 94.9%; Pred. No. 1e-105;
Matches 188; Conservative 0; Mismatches 9; Indel

QY 49 ELVHMINWAKRVPGFVDLTLDHQVHLLCAWLEILMIGLVWRSMEHH
Db 1 ELVHMINWAKRVPGFVDLTLDHQVHLLCAWLEILMIGLVWRSMEHH
QY 109 NQKCKVEGMVEIFDMLLATSSRFRMMNLQGEFVCLKSIILLNSGV
Db 61 NQKCKVEGMVEIFDMLLATSSRFRMMNLQGEFVCLKSIILLNSGV
QY 169 KDHIHRVLDKITDTLIHLMKAGLTQQQHQRLAQLLLILSHIRHM
Db 120 KDHIHRVLDKITDTLIHLMKAGLTQQQHQRLAQLLLILSHIRHM
QY 229 NVVPLYDLLLEMLDAHRL 246
Db 180 NVVPLYDLLLEMLDAHRL 197

RESULT 13
US-08-836-620A-9
; Sequence 9, Application US/08836620A
; Patent No. 5958710
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Orphan receptor
; NUMBER OF SEQUENCES: 19
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,620A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

```

APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-836-620A-9

Query Match 77.4%; Score 951.5; DB 2; Length 243;
Best Local Similarity 93.4%; Pred. No. 1.5e-104;
Matches 185; Conservative 2; Mismatches 10; Indels 1; Gaps 1;
QY 49 ELVHMINWAKRVPVGFVDTLTHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDR 108
Db 1 ELVHMINWAKRVPVGFVDTLTHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDR 60
QY 109 NQKCKVEGMVEIFDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEE 168
Db 61 NQKCKVEGMVEIFDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEE 119
QY 169 KDHIHRVLDKITDTLIHLMKAGLTLOQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCK 228
Db 120 KDHIHRVLDKITDTLIHLMKAGLTLOQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCK 179
QY 229 NVVPLYDLEMLDAHRL 246
Db 180 NVVPLYDLEMLDAHRL 197

RESULT 14
US-08-836-620A-8
Sequence 8, Application US/08836620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Rattus rattus
US-08-836-620A-8
Query Match 77.0%; Score 946.5; DB 2; Length 243;
Best Local Similarity 92.9%; Pred. No. 6e-104;
Matches 184; Conservative 2; Mismatches 11; Indels 1; Gaps 1;
QY 49 ELVHMINWAKRVPVGFVDTLTHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDR 108
Db 1 ELVHMINWAKRVPVGFVDTLTHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDR 60
QY 109 NQKCKVEGMVEIFDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEE 168
Db 61 NQKCKVEGMVEIFDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEE 119
QY 169 KDHIHRVLDKITDTLIHLMKAGLTLOQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCK 228
Db 120 KDHIHRVLDKITDTLIHLMKAGLTLOQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCK 179
QY 229 NVVPLYDLEMLDAHRL 246
Db 180 NVVPLYDLEMLDAHRL 197

RESULT 15
US-09-893-666A-2
Sequence 2, Application US/09893666A
Patent No. 6759568
GENERAL INFORMATION:
APPLICANT: YAMASHITA, ICHIRO
TITLE OF INVENTION: High estrogen-sensitive medaka fish
FILE REFERENCE: 210217US-620-7249-0
CURRENT APPLICATION NUMBER: US/09/893,666A
CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: JP 2000-247729
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 575
TYPE: PRT
ORGANISM: Oryzias latipes
US-09-893-666A-2

Query Match 64.4%; Score 792.5; DB 4; Length 575;
Best Local Similarity 63.0%; Pred. No. 3.9e-85;
Matches 155; Conservative 39; Mismatches 43; Indels 9; Gaps 2;
QY 5 SLTADQMVSAALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRVPGV 64
Db 268 SIPPEQVLLLLQGAEPPICLSRQKLSRPTYTEVTMTLLTSMADKELVHMIWAKKLPGL 327
QY 65 DLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCKVEGMVEIFDML 124
Db 328 QLSLDQVLLLESSWLEVLMIWRSIHCPGKLIFAQDLILDRNEGDCVEGTEIFDML 387
QY 125 LATSSRRFRMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDH-----IHRVLDKIT 180
Db 388 LATASRRFRVLKLPKEEFVCLKAILLNSGAFSFCGTGTM-----EPLHNSAAVQSMLEDTIT 442
QY 181 DTLIHLMAKAGLTLOQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLEML 240
Db 443 DALIHYISQSGYLAQEARRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLEML 502
QY 241 LDAHRL 246
Db 503 LDAHRL 508

Search completed: November 8, 2004, 08:29:28
Job time : 15.5592 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 8, 2004, 08:04:31 ; Search time 59.2408 Seconds
(without alignments)
1489.639 Million cell updates/sec

Title: US-09-830-693B-28
Perfect score: 1230
Sequence: 1 SLALSLTADQMVSALLDAEP.....CKNVVPLYDLLEMLDAHRL 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1206.5	98.1	414	AAE35275	Aae35275 C7LBDAS f
2	1206.5	98.1	422	AAB61498	Aab61498 Protein e
3	1206.5	98.1	438	AAE35276	Aae35276 C7LBDAS f
4	1206.5	98.1	457	AAB61499	Aab61499 Protein e
5	1206.5	98.1	480	AAB36684	Aab36684 Mammalian
6	1206.5	98.1	595	AAy21626	Aay21626 Ligand bi
7	1206.5	98.1	595	AAG84505	Aag84505 Human oes
8	1206.5	98.1	595	AAG84513	Aag84513 Human oes
9	1206.5	98.1	595	AAG84506	Aag84506 Human oes
10	1206.5	98.1	595	ABB76378	Abb76378 Human nuc
11	1206.5	98.1	595	ADP05661	Adp05661 Human nuc
12	1206.5	98.1	595	ADO42788	Ado42788 Wild type
13	1206.5	98.1	595	ADO42830	Ado42830 Human oes
14	1202.5	97.8	244	AAB26784	Aab26784 Oestrogen
15	1202.5	97.8	244	AAB26780	Aab26780 Human oes
16	1202.5	97.8	595	AAG84509	Aag84509 Human oes
17	1202.5	97.8	595	ADO42815	Ado42815 Mutant hu
18	1202	97.7	241	AAB26782	Aab26782 Oestrogen
19	1201.5	97.7	595	ADO42820	Ado42820 Mutant hu
20	1200.5	97.6	246	ABJ15106	Abj15106 LBDG1 rel
21	1200.5	97.6	595	AAG84507	Aag84507 Human oes
22	1200.5	97.6	595	ADO42789	Ado42789 Mutant hu
23	1199.5	97.5	595	AAG84508	Aag84508 Human oes
24	1199.5	97.5	595	AAG84514	Aag84514 Human oes
25	1198.5	97.4	595	AAG84512	Aag84512 Human oes

26	1198.5	97.4	660	5	ABB76379	Abb76379 Cre recom
27	1197.5	97.4	347	5	ABP70164	Abp70164 Amino aci
28	1197.5	97.4	414	6	AAE35278	Aae35278 C7LBDAS f
29	1197.5	97.4	438	6	AAE35281	Aae35281 C7LBDAS f
30	1197.5	97.4	511	7	ADE39222	Ade39222 LexA-oest
31	1197.5	97.4	547	5	AAU98984	Aau98984 Oestrogen
32	1197.5	97.4	589	7	ADB99352	Adb99352 Fusion pr
33	1197.5	97.4	595	2	AAy33506	Aay33506 Human est
34	1197.5	97.4	595	4	AAG84511	Aag84511 Human oes
35	1197.5	97.4	595	4	AAG84510	Aag84510 Human oes
36	1197.5	97.4	595	5	AAG68251	Aag68251 Human oes
37	1197.5	97.4	595	5	AAU98987	Aau98987 Oestrogen
38	1197.5	97.4	595	5	AAU98983	Aau98983 Oestrogen
39	1197.5	97.4	595	5	AAU98988	Aau98988 Oestrogen
40	1197.5	97.4	595	5	ABB09265	Abb09265 Human oes
41	1197.5	97.4	595	5	ABP70163	Abp70163 Amino aci
42	1197.5	97.4	595	5	ABB81783	Abb81783 Human oes
43	1197.5	97.4	595	6	ABG76090	Abg76090 Human oes
44	1197.5	97.4	595	6	ABR47448	AbR47448 Breast ca
45	1197.5	97.4	595	6	ABU09033	Abu09033 Human oes

ALIGNMENTS

RESULT 1
AAE35275
ID AAE35275 standard; protein; 414 AA.
XX
AC AAE35275;
XX
DT 28-MAY-2003 (first entry)
XX
DE C7LBDAS fusion (wild-type) protein.
XX
KW Oestrogen receptor; ER alpha; ligand binding domain; genetic disease;
KW acquired disease; cell proliferative disorder; cancer; adenocarcinoma;
KW LBD; gene switch; transgenic animal; transgenic; gene therapy; human;
KW zinc finger array; C7; fusion protein.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN WO200297050-A2.
XX
PD 05-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-US016946.
XX
PR 31-MAY-2001; 2001US-0294839P.
XX
PA (NOVS) NOVARTIS AG.
XX
PI Bracken KR, De Los Angeles JE, Huang Y, Kadan MJ, Ksander GM;
PI Zerby DB;
XX
DR WPI; 2003-156794/15.
DR N-PSDB; AAD53875.
XX
PT New mutant estrogen receptor ligand binding domain capable of interacting
PT with non-endogenous ligand, useful e.g. in combination with a ligand for
PT constructing selective molecular gene switches for regulating gene
PT function.
XX
PS Example 4; Page 117-118; 159pp; English.
XX
CC The invention relates to a mutant oestrogen receptor (ER) alpha-ligand
CC binding domain (LBD) which comprises an amino acid modification in region
CC 1, region 2 or both and interacting with a non-endogenous ligand as a
CC result of the amino acid modification. Sequences of the invention are
CC useful for treatment of genetic diseases, acquired diseases and any other
CC conditions including cell proliferative disorders such as cancer e.g.

CC The invention relates to a mutant oestrogen receptor (ER) alpha-ligand
CC binding domain (LBD) which comprises an amino acid modification in region
CC 1, region 2 or both and interacting with a non-endogenous ligand as a
CC result of the amino acid modification. Sequences of the invention are
CC useful for treatment of genetic diseases, acquired diseases and any other
CC conditions including cell proliferative disorders such as cancer e.g.
CC lung, breast, lymphoid, gastrointestinal, genito-urinary tract
CC adenocarcinomas and other malignancies such as colon cancers, renal- cell
CC carcinoma, prostate cancer, non-small cell carcinoma of the lung, cancer
CC of the small intestine and cancer of the oesophagus. The invention is
CC useful for constructing selective molecular gene switches for regulating
CC gene function in plants and transgenic animals. It is also useful in gene
CC therapy. The present sequence is human ER alpha LBD -zinc finger array
CC (C7) fusion protein
XX
SQ Sequence 438 AA;

Query Match 98.1%; Score 1206.5; DB 6; Length 438;
Best Local Similarity 96.3%; Pred. No. 2.3e-134;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 146 SLALSLTADQMVSAALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 205
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGEMVEI 120
Db 206 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGEMVEI 265
QY 121 FDMLLATSSRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHHRVLDKIT 180
Db 266 FDMLLATSSRFRMNLQGEFVCLKSIILLNSGVYTF-LSSSTLKSLEEKDHHRVLDKIT 324
QY 181 DTLIHLMAKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLLEM 240
Db 325 DTLIHLMAKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLLEM 384
QY 241 LDAHRL 246
Db 385 LDAHRL 390

RESULT 4
AAB61499
ID AAB61499 standard; protein; 457 AA.
XX
AC AAB61499;
XX 04-APR-2001 (first entry)
XX Protein encoded by human estrogen receptor alpha isoform #2.
DE
XX Human; estrogen receptor alpha; cancer; osteoporosis; bone; Alzheimer's;
KW cardiovascular.
XX Homo sapiens.
OS
XX WO200100823-A1.
PN
XX 04-JAN-2001.
PD
XX 27-JUN-2000; 2000WO-EP005981.
PF
XX 29-JUN-1999; 99IT-MI001433.
PR
XX (EUMO-) EURO MOLECULAR BIOLOGY LAB.
PA
XX Gannon F, Denger S, Flouriot G;
PI
XX WPI; 2001-137955/14.
DR
XX Novel isoforms of human estrogen receptor alpha useful for preparing
XX therapeutic agents for treating cancer, osteoporosis, Alzheimer's disease
PT

PT and cardiovascular diseases.
XX Claim 4; Page 46-48; 53pp; English.
PS
XX The present invention relates to a human estrogen receptor (hER)-alpha
CC isoform. Molecules which modulate the activity of the estrogen receptor
CC are useful for the preparation of therapeutic agents for treating cancer,
CC osteoporosis and other bone disorders, Alzheimer's disease and
CC cardiovascular diseases
XX
SQ Sequence 457 AA;

Query Match 98.1%; Score 1206.5; DB 4; Length 457;
Best Local Similarity 96.3%; Pred. No. 2.4e-134;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 167 SLALSLTADQMVSAALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 226
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGEMVEI 120
Db 227 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGEMVEI 286
QY 121 FDMLLATSSRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHHRVLDKIT 180
Db 287 FDMLLATSSRFRMNLQGEFVCLKSIILLNSGVYTF-LSSSTLKSLEEKDHHRVLDKIT 345
QY 181 DTLIHLMAKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLLEM 240
Db 346 DTLIHLMAKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLLEM 405
QY 241 LDAHRL 246
Db 406 LDAHRL 411

RESULT 5
AAB36684
ID AAB36684 standard; protein; 480 AA.
XX
AC AAB36684;
XX 15-MAR-2001 (first entry)
XX Mammalian two-hybrid protein SEQ ID NO:8.
DE
XX Mammalian; two-hybrid assay; hybrid protein; hybrid gene; detection;
KW reporter gene; DNA-binding region; transcriptional activation;
KW fused protein; protein interaction.
XX
OS Mammalia.
OS Synthetic.
XX
PN WO2000071743-A1.
XX 30-NOV-2000.
PD
XX 25-MAY-2000; 2000WO-JP003353.
PF
XX 25-MAY-1999; 99JP-00144946.
PR
XX (EISA) EISAI CO LTD.
PA
XX Tsukahara K, Hida T, Nakamura K, Yoshitomi H;
PI
XX WPI; 2001-025169/03.
DR N-PSDB; AAC88199.
XX
PT Novel two hybrid detection method comprising fusing two proteins with a
PT DNA binding sequence and a transcription activation sequence respectively
PT for detecting interaction of the proteins in mammalian cells.
XX

PS Example 2; Page 35-37; 63pp; Japanese.

XX

CC The present invention describes a method for detecting the interaction of

CC a first and a second protein within a mammalian cell. The method

CC comprises a fusion protein of the first protein with two or more

CC transcription activation sequences (which may be the same or different),

CC and a fusion protein of the second protein with a DNA-binding sequence.

CC These are expressed in a mammalian cell containing DNA carrying a

CC reporter gene downstream of a sequence binding to the DNA-binding

CC sequence; and the expression of the reporter gene is detected to indicate

CC interaction of the two proteins. The method is useful for the

CC identification and examination of potential interactions within the

CC mammalian cell, and screening of potential drugs targeting them. The

CC present sequence represents a hybrid protein from an example given in the

XX present invention

SQ Sequence 480 AA;

Query Match 98.1%; Score 1206.5; DB 4; Length 480;

Best Local Similarity 96.3%; Pred. No. 2.6e-134;

Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRV 60

Db 174 SLALSLTADQMVSAALLDAEPPILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRV 233

Qy 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEI 120

Db 234 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEI 293

Qy 121 FDMLLATSSRFRMMNLQGEFEVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 180

Db 294 FDMLLATSSRFRMMNLQGEFEVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 352

Qy 181 DTLIHLMAKAGLTQQQHQRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPVLYDLILEM 240

Db 353 DTLIHLMAKAGLTQQQHQRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPVLYDLILEM 412

Qy 241 LDAHRL 246

Db 413 LDAHRL 418

RESULT 6

AAY21626

ID AAY21626 standard; protein; 595 AA.

XX

AC AAY21626;

XX

DT 11-AUG-1999 (first entry)

XX

DE Ligand binding domain of nuclear receptor hER.

XX

KW Thyroid hormone receptor; aromatic compound; ligand binding domain;

KW alpha-glycerophosphate dehydrogenase; cardiac; obesity; triglyceride;

KW plasma cholesterol; anti-hypertriglyceridaemic; atherosclerosis; GPDH;

KW thyroid hormone replacement therapy; nuclear receptor.

XX

OS Homo sapiens.

XX

PN WO9926966-A2.

XX

PD 03-JUN-1999.

XX

PF 25-NOV-1998; 98WO-US025296.

XX

PR 26-NOV-1997; 97US-00980115.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Scanlan TS, Baxter JD, Fletcher RJ, Wagner RL, Kushner PJ;

PI Apriletti JW, West BL, Shiau AK;

XX

DR WPI; 1999-357810/30.

XX

PT Modulating activity of a thyroid hormone receptor.

XX

PS Disclosure; Fig 3G-R; 447pp; English.

XX

CC The invention relates to a method for modulating activity of a thyroid

CC hormone receptor that comprises administration of an aromatic compound

CC which fits spatially and preferentially into a thyroid hormone ligand

CC binding domain. The aromatic compound (of a specified formula) can be

CC used to increase alpha-glycerophosphate dehydrogenase (GPDH) levels, at

CC levels which do not significantly modify cardiac GPDH levels and are

CC indicated in the treatment of obesity. The compound also lower total

CC plasma cholesterol and triglyceride levels and can be used as anti-

CC hypertriglyceridaemic agents. The compound may also be used for treating

CC atherosclerosis and may be indicated in thyroid hormone replacement

CC therapy in patients with compromised cardiac function. Sequences AAY21621

CC - 636 amino acid sequences of ligand binding domains of several members

CC of the nuclear receptor superfamily

XX

SQ Sequence 595 AA;

Query Match 98.1%; Score 1206.5; DB 2; Length 595;

Best Local Similarity 96.3%; Pred. No. 3.5e-134;

Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRV 60

Db 305 SLALSLTADQMVSAALLDAEPPILYSEYDPTTRPFSEASMMGLLTNLADRELVHMINWAKRV 364

Qy 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEI 120

Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEI 424

Qy 121 FDMLLATSSRFRMMNLQGEFEVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 180

Db 425 FDMLLATSSRFRMMNLQGEFEVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483

Qy 181 DTLIHLMAKAGLTQQQHQRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPVLYDLILEM 240

Db 484 DTLIHLMAKAGLTQQQHQRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPVLYDLILEM 543

Qy 241 LDAHRL 246

Db 544 LDAHRL 549

RESULT 7

AAG84505

ID AAG84505 standard; protein; 595 AA.

XX

AC AAG84505;

XX

DT 10-SEP-2001 (first entry)

XX

DE Human oestrogen receptor alpha protein.

XX

KW Ligand dependent transcriptional factor; oestrogen receptor; ER;

KW glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;

KW MR; peroxisome proliferator-activated receptor protein; PPAR;

KW progesterone receptor protein; PR; pregnane X receptor protein; PXR;

KW thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;

KW transactivation; ERalpha; breast cancer.

XX

OS Homo sapiens.

XX

PN WO200142307-A1.

XX

PD 14-JUN-2001.

XX

PF 01-DEC-2000; 2000WO-JP008553.

XX

PR 07-DEC-1999; 99JP-00348022.

PR 27-DEC-1999; 99JP-00370667.
PR 07-JUL-2000; 2000JP-00207011.
PR 21-JUL-2000; 2000JP-00220508.
PR 02-AUG-2000; 2000JP-00234053.
PR 03-AUG-2000; 2000JP-00235460.
PR 03-AUG-2000; 2000JP-00235461.
PR 03-AUG-2000; 2000JP-00235463.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
XX Saito K, Ohe N, Satoh H;
PI WPI; 2001-367866/38.
XX
DR
XX
XX
PT Ligand dependent transcriptional factors, nucleic acids encoding them and
PT cells comprising them and a specified reporter gene, useful for screening
PT agents for the treatment of breast cancer.
XX
PS Claim 7; Page 167-170; 276pp; English.
XX
CC The present invention relates to ligand dependent transcriptional factors
CC including oestrogen receptor (ER) alpha and beta protein, glucocorticoid
CC receptor protein (GR), mineralocorticoid receptor protein (MR),
CC peroxisome proliferator-activated receptor protein (PPAR), progesterone
CC receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone
CC receptor protein (TR) and vitamin D receptor protein (VDR), the nucleic
CC acids encoding them and cells comprising them and a specified reporter
CC gene for the ligand dependent transcriptional factor. These proteins are
CC useful in the modulation of ligand dependent transcriptional factor
CC activity. The cells, mutant ERalpha and the polynucleotide encoding it
CC may be used in assays for qualitatively analysing an activity for
CC transactivation of a reporter gene by a test ERalpha, for screening
CC mutant ligand dependent transcriptional factors, for evaluating an
CC activity for transactivation of a reporter gene by a test ERalpha and/or
CC for screening a compound useful for treating a disorder of a mutant
CC ERalpha, especially breast cancer
XX
SQ Sequence 595 AA;

Query Match 98.1%; Score 1206.5; DB 4; Length 595;
Best Local Similarity 96.3%; Pred. No. 3.5e-134;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSALLDAEPPILYSEYDPTFPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSALLDAEPPILYSEYDPTFPFSEASMMGLLTNLADRELVHMINWAKRV 364

QY 61 PGFVDLTLDHQQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 120
Db 365 PGFVDLTLDHQQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 424

QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEKDHIHRVLDKIT 180
Db 425 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTF-LSSSTLKSLEEKDHIHRVLDKIT 483

QY 181 DTLIHLMAGAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLLEM 240
Db 484 DTLIHLMAGAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLLEM 543

QY 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 8
AAG84513
ID AAG84513 standard; protein; 595 AA.
XX
AC AAG84513;
XX
XT 10-SEP-2001 (first entry)
XX
DE Human oestrogen receptor alpha protein mutant S578P.

XX
KW Ligand dependent transcriptional factor; oestrogen receptor; ER;
KW glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;
KW MR; peroxisome proliferator-activated receptor protein; PPAR;
KW progesterone receptor protein; PR; pregnane X receptor protein; PXR;
KW thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;
KW transactivation; ERalpha; breast cancer; mutant; mutein.
XX
OS Homo sapiens.
XX
XX WO200142307-A1.
XX
XX 14-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-JP008553.
PF
XX
PR 07-DEC-1999; 99JP-00348022.
PR 27-DEC-1999; 99JP-00370667.
PR 07-JUL-2000; 2000JP-00207011.
PR 21-JUL-2000; 2000JP-00220508.
PR 02-AUG-2000; 2000JP-00234053.
PR 03-AUG-2000; 2000JP-00235460.
PR 03-AUG-2000; 2000JP-00235461.
PR 03-AUG-2000; 2000JP-00235463.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
XX Saito K, Ohe N, Satoh H;
PI WPI; 2001-367866/38.
XX
PT Ligand dependent transcriptional factors, nucleic acids encoding them and
PT cells comprising them and a specified reporter gene, useful for screening
PT agents for the treatment of breast cancer.
XX
PS Claim 20; Page 194-197; 276pp; English.
XX
CC The present invention relates to ligand dependent transcriptional factors
CC including oestrogen receptor (ER) alpha and beta protein, glucocorticoid
CC receptor protein (GR), mineralocorticoid receptor protein (MR),
CC peroxisome proliferator-activated receptor protein (PPAR), progesterone
CC receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone
CC receptor protein (TR) and vitamin D receptor protein (VDR), the nucleic
CC acids encoding them and cells comprising them and a specified reporter
CC gene for the ligand dependent transcriptional factor. These proteins are
CC useful in the modulation of ligand dependent transcriptional factor
CC activity. The cells, mutant ERalpha and the polynucleotide encoding it
CC may be used in assays for qualitatively analysing an activity for
CC transactivation of a reporter gene by a test ERalpha, for screening
CC mutant ligand dependent transcriptional factors, for evaluating an
CC activity for transactivation of a reporter gene by a test ERalpha and/or
CC for screening a compound useful for treating a disorder of a mutant
CC ERalpha, especially breast cancer
XX
SQ Sequence 595 AA;

Query Match 98.1%; Score 1206.5; DB 4; Length 595;
Best Local Similarity 96.3%; Pred. No. 3.5e-134;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSALLDAEPPILYSEYDPTFPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSALLDAEPPILYSEYDPTFPFSEASMMGLLTNLADRELVHMINWAKRV 364

QY 61 PGFVDLTLDHQQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 120
Db 365 PGFVDLTLDHQQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 424

QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEKDHIHRVLDKIT 180
Db 425 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTF-LSSSTLKSLEEKDHIHRVLDKIT 483

QY 181 DTLIHLMAGAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLLEM 240

|||||
484 DTLIHLMKAGLTQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKNVVPLYDLLLLL 543
241 LDAHRL 246
544 LDAHRL 549
RESULT 9
AAG84506
ID AAG84506 standard; protein; 595 AA.
XX
AC AAG84506;
XX
DT 10-SEP-2001 (first entry)
XX Human oestrogen receptor alpha protein mutant K303R.
DE
XX
KW Ligand dependent transcriptional factor; oestrogen receptor; ER;
KW glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;
KW ER; peroxisome proliferator-activated receptor protein; PPAR;
KW progesterone receptor protein; PR; pregnane X receptor protein; PXR;
KW thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;
KW transactivation; ERalpha; breast cancer; mutant; mutein.
XX
OS Homo sapiens.
XX
PN WO200142307-A1.
XX
PD 14-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-JP008553.
XX
PR 07-DEC-1999; 99JP-00348022.
PR 27-DEC-1999; 99JP-00370667.
PR 07-JUL-2000; 2000JP-00207011.
PR 21-JUL-2000; 2000JP-00220508.
PR 02-AUG-2000; 2000JP-00234053.
PR 03-AUG-2000; 2000JP-00235460.
PR 03-AUG-2000; 2000JP-00235461.
PR 03-AUG-2000; 2000JP-00235463.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
XX
PI Saito K, Ohe N, Satoh H;
XX
DR WPI; 2001-367866/38.
XX
XX
PT Ligand dependent transcriptional factors, nucleic acids encoding them and
PT cells comprising them and a specified reporter gene, useful for screening
PT agents for the treatment of breast cancer.
XX
PS Claim 15; Page 170-174; 276pp; English.
XX
CC The present invention relates to ligand dependent transcriptional factors
CC including oestrogen receptor (ER) alpha and beta protein, glucocorticoid
CC receptor protein (GR), mineralocorticoid receptor protein (MR),
CC peroxisome proliferator-activated receptor protein (PPAR), progesterone
CC receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone
CC receptor protein (TR), and vitamin D receptor protein (VDR), the nucleic
CC acids encoding them and cells comprising them and a specified reporter
CC gene for the ligand dependent transcriptional factor. These proteins are
CC useful in the modulation of ligand dependent transcriptional factor
CC activity. The cells, mutant ERalpha and the polynucleotide encoding it
CC may be used in assays for qualitatively analysing an activity for
CC transactivation of a reporter gene by a test ERalpha, for screening
CC mutant ligand dependent transcriptional factors, for evaluating an
CC activity for transactivation of a reporter gene by a test ERalpha and/or
CC for screening a compound useful for treating a disorder of a mutant
CC ERalpha, especially breast cancer
XX
SQ Sequence 595 AA;

Query Match 98.1%; Score 1206.5; DB 4; Length 595;
Best Local Similarity 96.3%; Pred. No. 3.5e-134;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEI 120
Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVEGMVEI 424
QY 121 FDMLLATSSRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXEKKDHIHRVLDKIT 180
Db 425 FDMLLATSSRFRMNLQGEFVCLKSIILLNSGVYTF-LSSSTLKSLEEKDHIHRVLDKIT 483
QY 181 DTLIHLMKAGLTQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKNVVPLYDLLLLL 240
Db 484 DTLIHLMKAGLTQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMCKNVVPLYDLLLLL 543
QY 241 LDAHRL 246
Db 544 LDAHRL 549
RESULT 10
ABB76378
ID ABB76378 standard; protein; 595 AA.
XX
AC ABB76378;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human nuclear oestrogen receptor alpha.
XX
KW Oestrogen; receptor; human; transgenic mouse; cytostatic;
KW antiinflammatory; antidiabetic; endocrine; anorectic; hepatotropic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 180..262 /note= "DNA-binding domain"
FT Region 263..301 /note= "D hinge region"
FT Domain 302..552 /note= "ligand-binding domain"
XX
PN WO200228175-A2.
XX
PD 11-APR-2002.
XX
PF 28-SEP-2001; 2001WO-IB002246.
XX
PR 03-OCT-2000; 2000FR-00012570.
PR 11-MAY-2001; 2001US-00853033.
XX
PA (ADER-) ADEREGEM ASSOC DEV RECH EN GENETIQ.
XX
PI Chambon P, Metzger D;
XX
DR WPI; 2002-463217/49.
DR N-PSDB; ABL57497.
XX
PT A transgenic mouse, useful in screening for medicaments for the treatment
PT of e.g., diabetes or skin cancers, comprises a fusion protein between a
PT recombinase Cre, and a modified ligand binding domain of the nuclear
PT estrogen receptor alpha.
XX
PS Claim 6; Page 131-132; 149pp; English.
XX
CC The present sequence is the protein sequence of the human nuclear
CC oestrogen receptor alpha (I). The invention relates to a non-human

CC metazoan organism, especially a transgenic mouse, characterised in that
CC at least one cell comprises: (i) a fusion protein formed from a
CC recombinase (Cre), a hinge region (preferably human (I) D hinge), and a
CC modified ligand binding domain (LBD) of a nuclear oestrogen receptor,
CC especially human (I), its fragment or variant; and (ii) one or more genes
CC or DNA sequences of interest belonging to the genome of the organism,
CC into which one or more recognition sites of the recombinase protein are
CC inserted. The (I) LBD domain is preferably modified by a G521R, G400V, or
CC M543A/L544A mutation. The fusion protein has negligible, or even zero,
CC recombinase activity in the presence of a natural ligand such as
CC oestradiol, but recombinase activity is induced by a small quantity of a
CC synthetic ligand that has antioestrogenic activity, e.g. tamoxifen or 4-
CC hydroxytamoxifen. The metazoan organism or its cells, such as epidermal
CC cells, hepatocytes or adipocytes, are useful in carrying out a
CC spatiotemporally controlled site-specific recombination of a DNA sequence
CC of interest in its natural chromatin environment. It is also used in
CC screening of medicaments for pathological conditions associated with an
CC alteration of the expression and/or function of the DNA sequence of
CC interest, such as skin cancer, inflammation, diabetes, alopecia, obesity,
CC or in promoting hepatic regeneration

XX SQ Sequence 595 AA;

Query Match 98.1%; Score 1206.5; DB 5; Length 595;
Best Local Similarity 96.3%; Pred. No. 3.5e-134;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPSEASMMGLLTNLADRELVHMINKRV 60
Db |||||
305 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPSEASMMGLLTNLADRELVHMINKRV 364
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120
Db |||||
365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 424
QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIIILNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db |||||
425 FDMLLATSSRRFRMNLQGEFVCLKSIIILNSGVYTF-LSSSTLKSLEEKDHIHRVLDKIT 483
QY 181 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDYLLEM 240
Db |||||
484 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDYLLEM 543
QY 241 LDAHRL 246
Db |||||
544 LDAHRL 549

ADP05661 standard; protein; 595 AA.

AC ADP05661;

XX 26-AUG-2004 (first entry)

DE Human nuclear receptor protein SeqID35.

XX disease risk; disorder risk; mutation; polymorphism;
KW nuclear receptor protein; antibacterial; antithyroid; cardiovascular-Gen;
KW cytostatic; dermatological; eating-Disorders-Gen; gastrointestinal-Gen;
KW gynaecological; hepatotropic; immunosuppressive; muscular-Gen;
KW nephrotropic; osteopathic; virucide; adrenal gland; colon;
KW cardiovascular; intestine; kidney; liver; lung; muscular; ovary; blood;
KW prostate; skin; spleen; stomach; testes; thymus; thyroid; uterus;
KW pancreas; bone; joint; breast; immune system; metabolic;
KW nutritive disease; human.

XX Homo sapiens.

XX WO2004045369-A2.

XX 03-JUN-2004.

XX 12-NOV-2003; 2003WO-US036229.
XX 14-NOV-2002; 2002US-0426305P.
XX (NURA-) NURA INC.
XX Gaitanaris GA, Bergmann JE, Gracarov A, Hohmann J, Li F;
PI Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX WPI; 2004-449627/42.
XX N-PSDB; ADP05662.
PT Determining an increased risk for e.g. colon, brain or breast disease or
PT disorder, by detecting a mutation or polymorphism in the nuclear receptor
PT gene, or measuring expression or biological activity level of the nuclear
PT receptor.
XX Claim 1; SEQ ID NO 35; 508pp; English.

CC This invention relates to a novel method of determining whether a patient
CC has an increased risk for developing a disease or disorder which
CC comprises determining the presence of a mutation or polymorphism in the
CC patient's gene encoding a nuclear receptor protein or measuring the
CC expression or level of biological activity of a nuclear receptor
CC polypeptide in the patient or in a cell of the patient. The invention may
CC be useful for the development of compounds with an antibacterial,
CC antithyroid, cardiovascular-Gen, cytostatic, dermatological, eating-
CC Disorders-Gen, gastrointestinal-Gen, gynaecological, hepatotropic,
CC immunosuppressive, muscular-Gen, nephrotropic, osteopathic or virucide
CC activity. The method is useful for determining whether a patient has an
CC increased risk for developing a disease or disorder. The nucleic acid
CC encoding a nuclear receptor polypeptide, an expression vector comprising
CC the nucleic acid operably linked to a promoter, or a compound that
CC modulates the biological activity of a nuclear receptor polypeptide, is
CC useful for treating or preventing a disease or disorder of the adrenal
CC gland, colon, cardiovascular, intestine, kidney, liver, lung, muscular,
CC ovary, blood, prostate, skin, spleen, stomach, testes, thymus, thyroid,
CC uterus, pancreas, bone and joints, breast, or immune system, or metabolic
CC or nutritive disease or disorder. The present sequence is that of a
CC nuclear receptor protein which may be used in the method of the
CC invention.

XX SQ Sequence 595 AA;

Query Match 98.1%; Score 1206.5; DB 8; Length 595;
Best Local Similarity 96.3%; Pred. No. 3.5e-134;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPSEASMMGLLTNLADRELVHMINKRV 60
Db |||||
305 SLALSLTADQMVSAALLDAEPPILYSEYDPTRPSEASMMGLLTNLADRELVHMINKRV 364
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120
Db |||||
365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 424
QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIIILNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db |||||
425 FDMLLATSSRRFRMNLQGEFVCLKSIIILNSGVYTF-LSSSTLKSLEEKDHIHRVLDKIT 483
QY 181 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDYLLEM 240
Db |||||
484 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDYLLEM 543
QY 241 LDAHRL 246
Db |||||
544 LDAHRL 549

RESULT 12
ADO42788
ID ADO42788 standard; protein; 595 AA.

XX ADO42788;
AC 26-AUG-2004 (first entry)
XX
DT
XX
DE
XX
DE Wild type human oestrogen receptor-alpha (ER) protein.
XX
KW human; oestrogen receptor-alpha; ER; ER activity regulator substance;
KW anti-oestrogen substance.
XX
OS Homo sapiens.
XX
PN WO2004046352-A1.
XX
PD 03-JUN-2004.
XX
PF 14-NOV-2003; 2003WO-JP014494.
XX
PR 15-NOV-2002; 2002JP-00331994.
XX
PR 15-NOV-2002; 2002JP-00331995.
XX
PR 15-NOV-2002; 2002JP-00331996.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
PI Fujimori K;
XX
XX WPI; 2004-431978/40.
XX
DR New mutant estrogen receptor-alpha useful for determining effectiveness
PT of treatment by estrogen receptor activity regulator substance and
PT antiestrogen substance.
PT
XX
XX Claim 1; SEQ ID NO 1; 111pp; Japanese.
PS
XX The invention comprises the amino acid sequences of mutant human
XX oestrogen receptor-alpha (ER) proteins. The mutant ER proteins of the
CC invention are useful for determining the effectiveness of a treatment by
CC an ER activity regulator substance, and for determining the effectiveness
CC of a treatment by an anti-oestrogen substance. The present amino acid
CC sequence represents the wild-type human ER protein.
XX
SQ Sequence 595 AA;

Query Match 98.1%; Score 1206.5; DB 8; Length 595;
Best Local Similarity 96.3%; Pred. No. 3.5e-134;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 SLALSITADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
DB 305 SLALSITADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 364

QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVGMEVEI 120
DB 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVGMEVEI 424

QY 121 FDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKHHRVLDKIT 180
DB 425 FDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483

QY 181 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEEM 240
DB 484 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEEM 543

QY 241 LDAHRL 246
DB 544 LDAHRL 549

RESULT 13
ADO42830
ID ADO42830 standard; protein; 595 AA.
XX
AC ADO42830;

Query Match 98.1%; Score 1206.5; DB 8; Length 595;
Best Local Similarity 96.3%; Pred. No. 3.5e-134;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 SLALSITADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
DB 305 SLALSITADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 364

QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVGMEVEI 120
DB 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVGMEVEI 424

QY 121 FDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKHHRVLDKIT 180
DB 425 FDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483

QY 181 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEEM 240
DB 484 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEEM 543

QY 241 LDAHRL 246
DB 544 LDAHRL 549

RESULT 14
AAB26784
ID AAB26784 standard; protein; 244 AA.
XX
AC AAB26784;
DT 18-JAN-2001 (first entry)

XX 26-AUG-2004 (first entry)
DT
XX
DE Human oestrogen receptor-alpha (ER) protein.
XX
KW human; oestrogen receptor-alpha; ER; ER activity regulator substance;
KW anti-oestrogen substance.
XX
OS Homo sapiens.
XX
PN WO2004046352-A1.
XX
PD 03-JUN-2004.
XX
PF 14-NOV-2003; 2003WO-JP014494.
XX
PR 15-NOV-2002; 2002JP-00331994.
PR 15-NOV-2002; 2002JP-00331995.
PR 15-NOV-2002; 2002JP-00331996.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
PI Fujimori K;
XX
XX WPI; 2004-431978/40.
XX
DR New mutant estrogen receptor-alpha useful for determining effectiveness
PT of treatment by estrogen receptor activity regulator substance and
PT antiestrogen substance.
PT
XX
XX Disclosure; Fig 19; 111pp; Japanese.
PS
XX The invention comprises the amino acid sequences of mutant human
CC oestrogen receptor-alpha (ER) proteins. The mutant ER proteins of the
CC invention are useful for determining the effectiveness of a treatment by
CC an ER activity regulator substance, and for determining the effectiveness
CC of a treatment by an anti-oestrogen substance. The present amino acid
CC sequence represents a human ER protein.
XX
SQ Sequence 595 AA;

Query Match 98.1%; Score 1206.5; DB 8; Length 595;
Best Local Similarity 96.3%; Pred. No. 3.5e-134;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 SLALSITADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
DB 305 SLALSITADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 364

QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVGMEVEI 120
DB 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQKCVGMEVEI 424

QY 121 FDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKHHRVLDKIT 180
DB 425 FDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483

QY 181 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEEM 240
DB 484 DTLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDLLEEM 543

QY 241 LDAHRL 246
DB 544 LDAHRL 549

RESULT 14
AAB26784
ID AAB26784 standard; protein; 244 AA.
XX
AC AAB26784;
DT 18-JAN-2001 (first entry)

XX Oestrogen receptor protein sequence.

DE Homology model; ligand binding domain; glucocorticoid receptor; AIDS;

XX hypertension; diabetes; obesity; glaucoma; depression; wound;

KW protein co-ordinate data; thyroid hormone receptor; oestrogen receptor.

KW Unidentified.

XX WO200052050-A2.

PN 08-SEP-2000.

XX 01-MAR-2000; 2000WO-GB000727.

PF 01-MAR-1999; 99GB-00004441.

XX 22-APR-1999; 99GB-00009151.

XX (KARO-) KARO BIO AB.

PA Gillner M, Greenidge P;

XX WPI; 2000-549565/50.

DR Designing a homology model of the ligand binding domain of a

XX glucocorticoid receptor displayed as a three-dimensional image, useful

PT for identifying agonists and antagonists for treating e.g. inflammation,

PT hypertension, glaucoma, diabetes.

XX Disclosure; Fig 6; 246pp; English.

PS This invention relates to a method for designing an homology model of the

XX ligand binding domain of a glucocorticoid receptor. The homology model

CC may be displayed as a three-dimensional image. The method comprises: (a)

CC providing an amino acid sequence and an x-ray crystallographic structure

CC of the ligand binding domain of a thyroid, oestrogen or progesterone

CC receptor; (b) modifying the x-ray crystallographic structure to take

CC account of differences between the amino acid configuration of the ligand

CC binding domain of the glucocorticoid receptor and the thyroid, oestrogen,

CC or progesterone receptor; (c) verifying the accuracy of the homology

CC model by comparing it with experimentally-determined binding properties

CC of a number of ligands for the glucocorticoid receptor; and (d) modifying

CC the homology model for greater consistency with the binding properties.

CC The homology model is useful for drug screening and designing ligands

CC (agonists and antagonists) capable of binding to a glucocorticoid

CC receptor. The identified agonists are useful for the treatment of

CC inflammation and also in immunosuppressive therapy. The identified

CC antagonists are useful for the treatment of hypertension, diabetes,

CC obesity, glaucoma, depression, acquired immune deficiency syndrome (AIDS)

CC and wounds. The homology models are also useful for electronic screening

CC of compound databases, de novo drug design and/or prediction of binding

CC affinities of glucocorticoid receptor ligands for the receptor by

CC molecular mechanics scoring functions. The specification contains protein

CC co-ordinate data for the glucocorticoid receptor models produced using

CC the method, based on the X-ray crystallographic structure of the

CC oestrogen and progesterone receptors. The present sequence represents an

CC oestrogen receptor protein. The protein is used in an example of the

CC method of the invention for homology modelling of a glucocorticoid

CC receptor based on the thyroid and oestrogen receptors

XX Sequence 244 AA;

SQ

Query Match 97.8%; Score 1202.5; DB 3; Length 244;

Best Local Similarity 96.3%; Pred. No. 3e-134;

Matches 236; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMVSAALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60

Db 1 SLALSLTADQMVSAALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60

Qy 61 PGFVDTLHDQVHLLCAWLEILMTGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEV 120

Db 61 PGFVDTLHDQVHLLCAWLEILMTGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEV 120

Qy 121 FDMLLATSSRRFMNLOGEFVCLKSIILLNSGVYTFXXXXXXXEEDKHHRVLDKIT 180

Db 121 FDMLLATSSRRFMNLOGEFVCLKSIILLNSGVYTF-LSSTLSLEEKDHIHRVLDKIT 179

Qy 181 DTLIHLMKAGLTLOQOQHQRALQALLLILSHIRHMSNKGMEHLYSMCKNVVPLYDLLEM 240

Db 180 DTLIHLMKAGLTLOQOQHQRALQALLLILSHIRHMSNKGMEHLYSMCKNVVPLYDLLEM 239

Qy 241 LDAH 245

Db 240 LDAH 244

RESULT 15

AAB26780

ID AAB26780 standard; protein; 244 AA.

XX

AC AAB26780;

XX

DT 18-JAN-2001 (first entry)

DE Human oestrogen receptor protein sequence.

XX

KW Homology model; ligand binding domain; glucocorticoid receptor; AIDS;

KW hypertension; diabetes; obesity; glaucoma; depression; wound; human;

KW protein co-ordinate data; thyroid hormone receptor; oestrogen receptor.

XX

OS Homo sapiens.

XX WO200052050-A2.

PN 08-SEP-2000.

XX

PF 01-MAR-2000; 2000WO-GB000727.

XX

PR 01-MAR-1999; 99GB-00004441.

PR 22-APR-1999; 99GB-00009151.

XX

PA (KARO-) KARO BIO AB.

XX

PI Gillner M, Greenidge P;

XX WPI; 2000-549565/50.

XX

PT Designing a homology model of the ligand binding domain of a

PT glucocorticoid receptor displayed as a three-dimensional image, useful

PT for identifying agonists and antagonists for treating e.g. inflammation,

PT hypertension, glaucoma, diabetes.

XX

PS Disclosure; Fig 2A; 246pp; English.

XX

CC This invention relates to a method for designing an homology model of the

CC ligand binding domain of a glucocorticoid receptor. The homology model

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CC human oestrogen receptor protein. The protein is used in an example of
CC the method of the invention for homology modelling based on the thyroid
CC receptor
XX
SQ Sequence 244 AA;

Query Match 97.8%; Score 1202.5; DB 3; Length 244;
Best Local Similarity 96.3%; Pref. No. 3e-134;
Matches 236; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy	1	SLALSLTADQMVSA	LLDAEPPILYSEYDPT	RPFFSEASMMGLLT	NLADRELVHM	INWAKRV	60
Db	1	SLALSLTADQMVSA	LLDAEPPILYSEYDPT	RPFFSEASMMGLLT	NLADRELVHM	INWAKRV	60
Qy	61	PGFVDLT	LHDQVHLL	ECANLEILMIGLV	WRSMEHPGKLL	FAPNLL	LLDRNQK
Db	61	PGFVDLT	LHDQVHLL	ECANLEILMIGLV	WRSMEHPGKLL	FAPNLL	LLDRNQK
Qy	121	FDMLLATSS	RFRMMNLQGE	EFVCLKSI	ILLNSGVYTF	XXXXXXXXXX	EEDKH
Db	121	FDMLLATSS	RFRMMNLQGE	EFVCLKSI	ILLNSGVYTF	XXXXXXXXXX	EEDKH
Qy	181	DTLIHLM	AKAGLT	LQQQHQR	LAQLLL	ILSHIRH	MSNKGMEHLY
Db	180	DTLIHLM	AKAGLT	LQQQHQR	LAQLLL	ILSHIRH	MSNKGMEHLY
Qy	241	LDAHR	245				
Db	240	LDAHR	244				

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Job time : 59.2408 secs